



**Weill Cornell
Medicine**



Weill Cornell Medicine
Institute of Artificial Intelligence
for Digital Health

Disentangling the Clinical Complexity of Heterogeneous Diseases Through Data-Driven Subphenotyping with Large Scale Electronic Health Records

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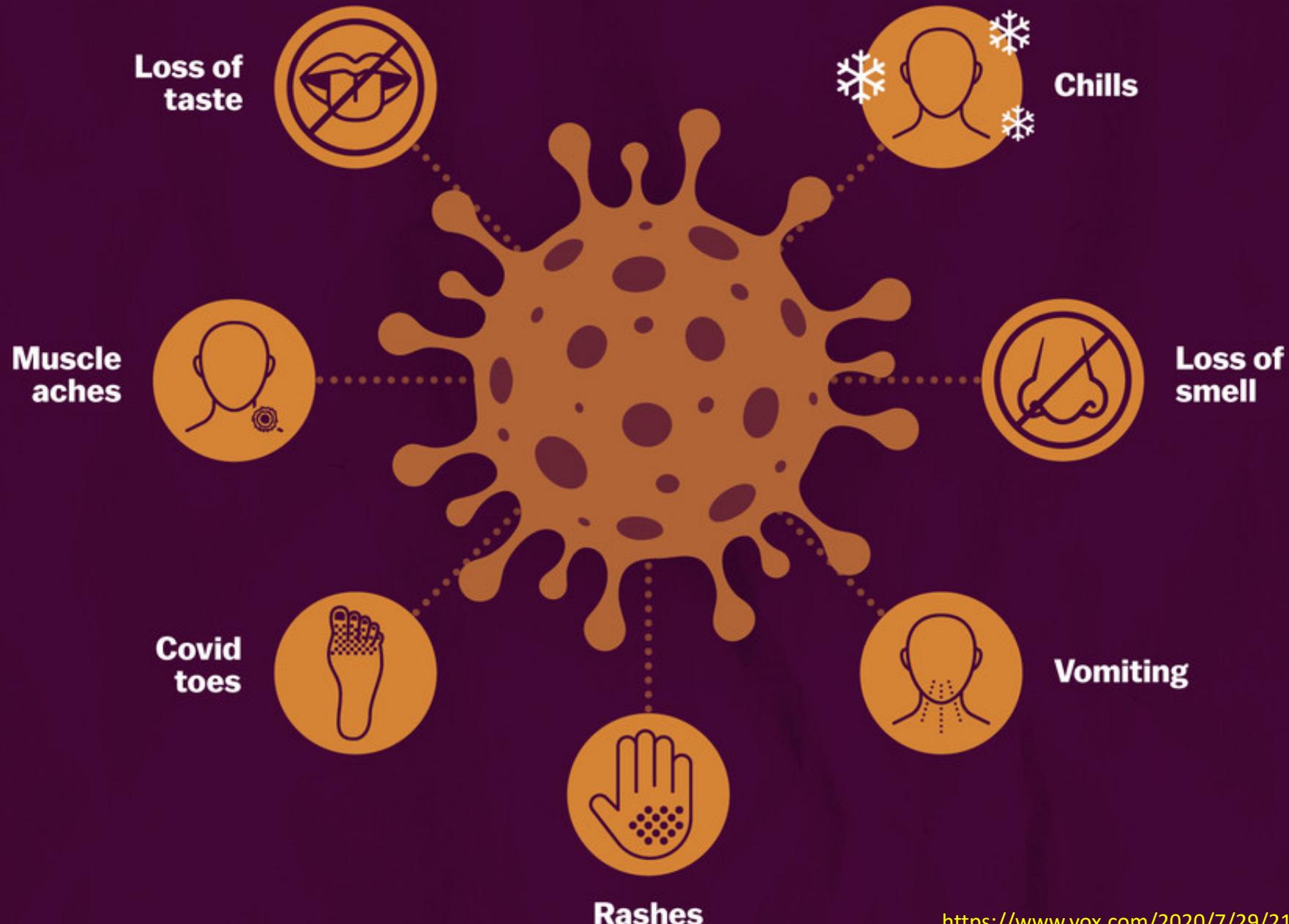
<https://wcm-wanglab.github.io/index.html>

Outline

- Introduction
- Subphenotyping of COVID-19 at infection confirmation
- Subphenotyping of Severe COVID-19 after Mechanical Ventilation
- Subphenotyping of Long COVID
- Discussions

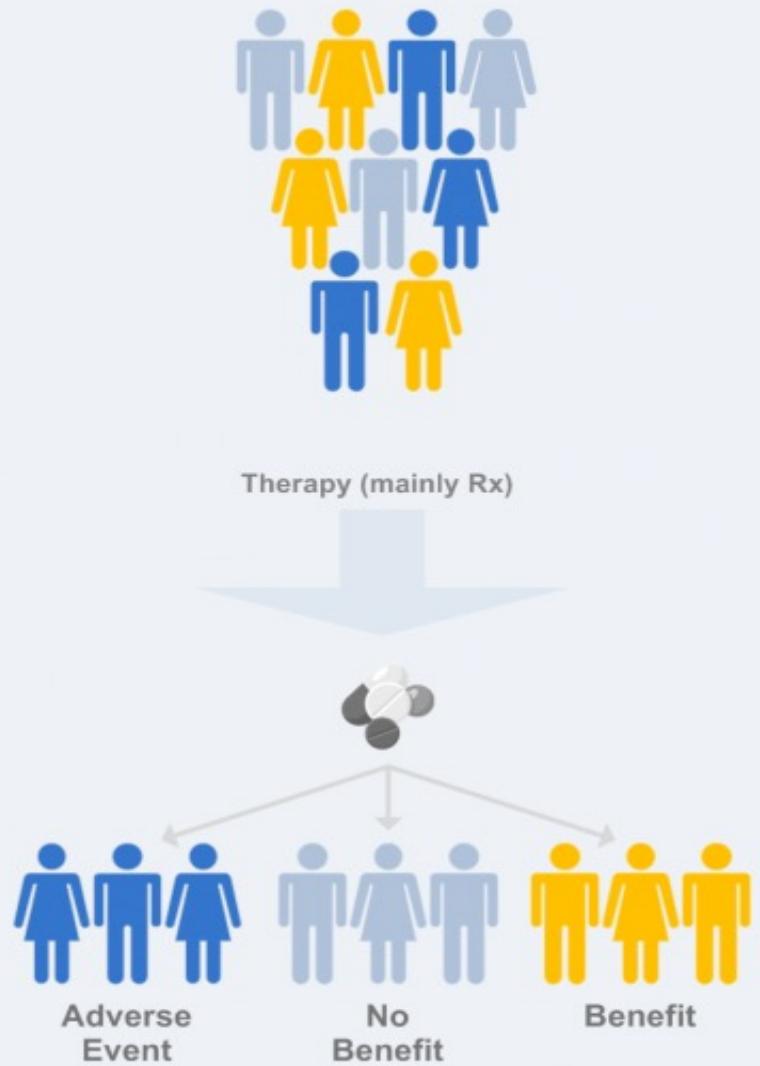
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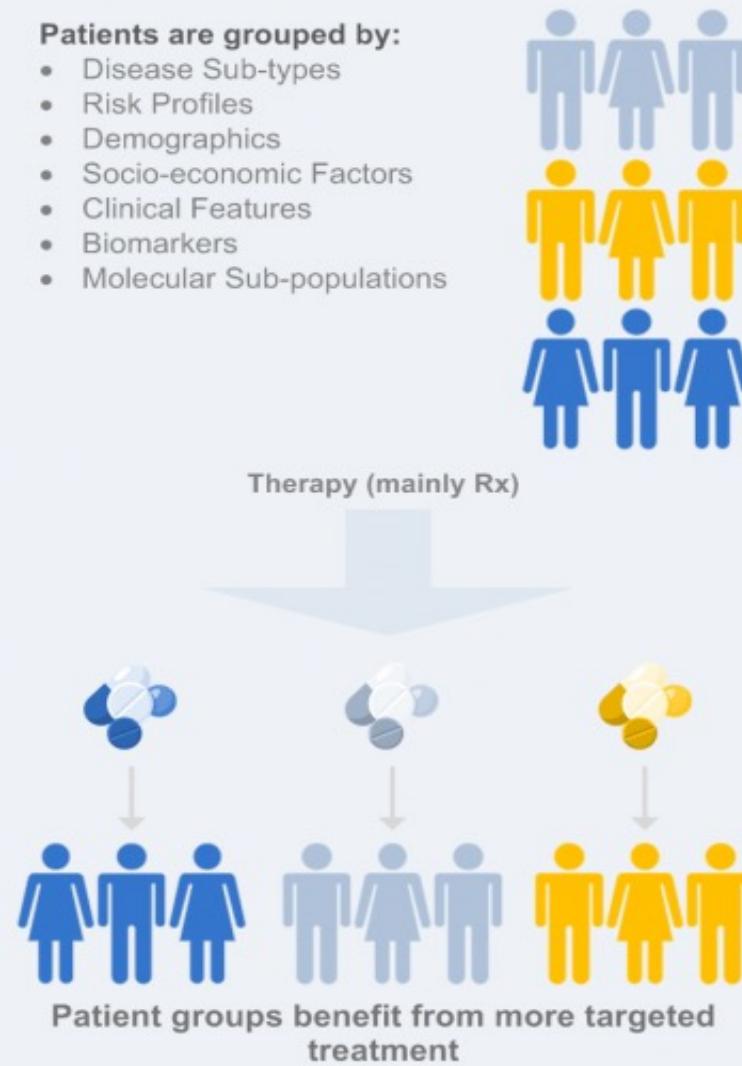
Traditional Medicine



Stratified Medicine

Patients are grouped by:

- Disease Sub-types
- Risk Profiles
- Demographics
- Socio-economic Factors
- Clinical Features
- Biomarkers
- Molecular Sub-populations



Precision Medicine

Individual patient level:

- Genomics and Omics
- Lifestyle
- Preferences
- Health History
- Medical Records
- Compliance
- Exogenous Factors



Therapy (Rx + Dx = CDx)



Precision medicine research enables development and delivery of the right patient intervention

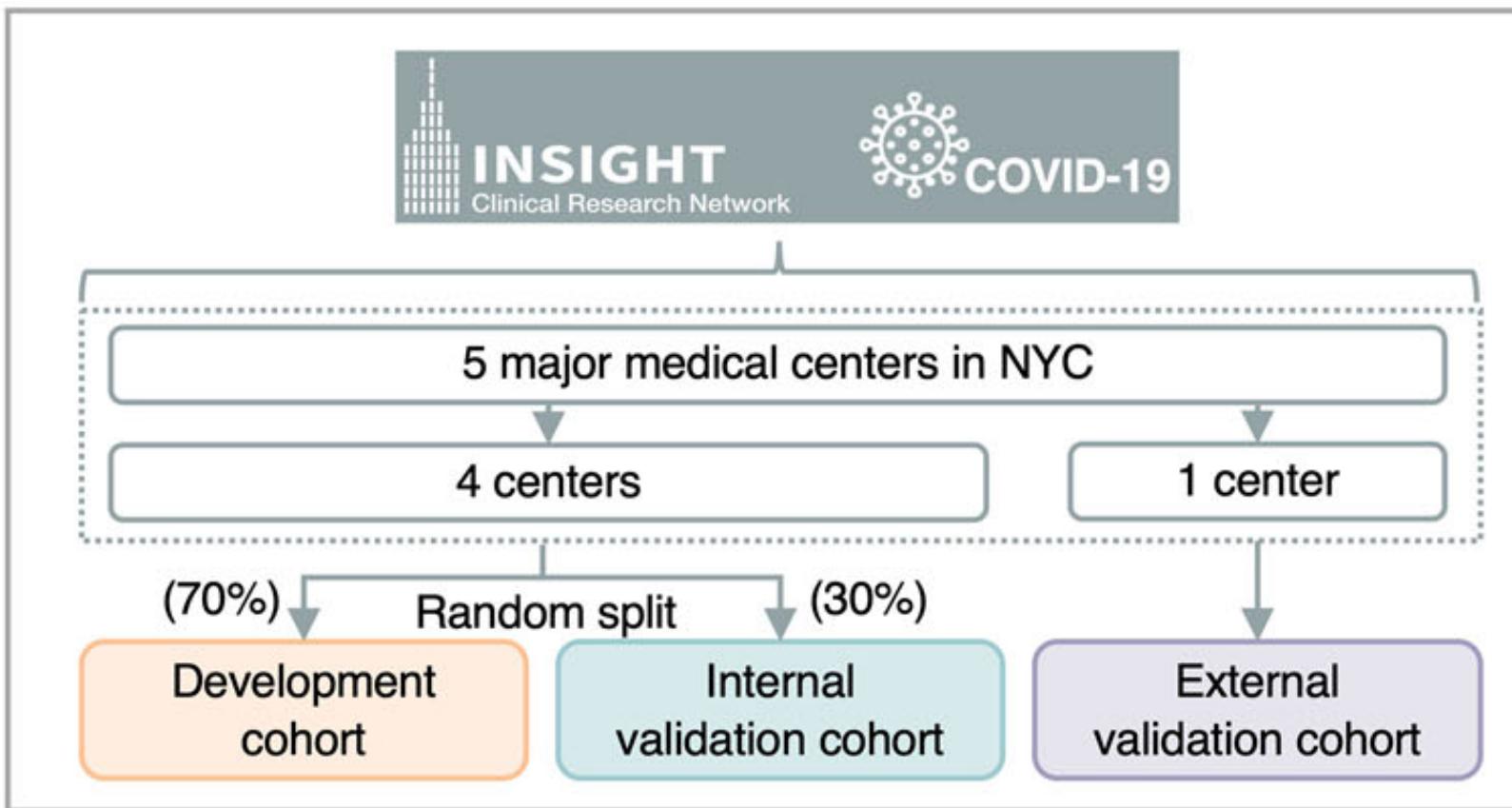
<https://www.linguamatics.com/solutions/precision-medicine>

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- Introduction
- Subphenotyping of COVID-19 at infection confirmation
- Subphenotyping of Severe COVID-19 after Mechanical Ventilation
- Subphenotyping of Long COVID
- Subphenotyping of AD
- Discussions

Su, Chang, Yongkang Zhang, James H. Flory, Mark G. Weiner, Rainu Kaushal, Edward J. Schenck, and Fei Wang. "Clinical subphenotypes in COVID-19: derivation, validation, prediction, temporal patterns, and interaction with social determinants of health." *NPJ digital medicine* 4, no. 1 (2021): 110.

Overall Setup



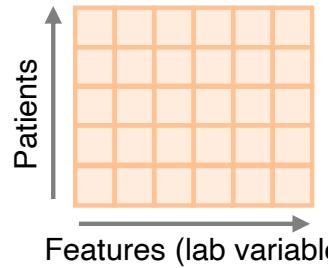
Data preparation



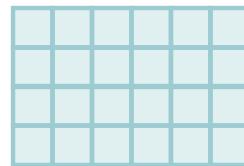
- Collection of presenting laboratory test data;
- Data scaling;
- Imputation of missing data



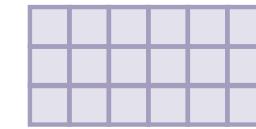
Development cohort



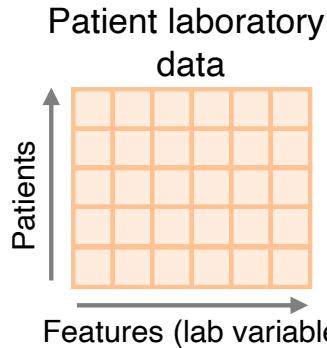
Internal validation cohort
External validation cohort



External validation cohort

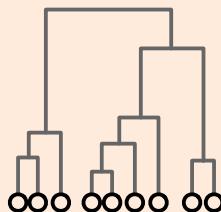


Derivation of subphenotypes



Development cohort

Agglomerative hierarchical clustering



...

Subphenotypes (i.e., patient subgroups)

Sensitivity analysis

Development cohort

1. Sensitivity to outliers

Re-deriving subphenotypes after removing outliers.

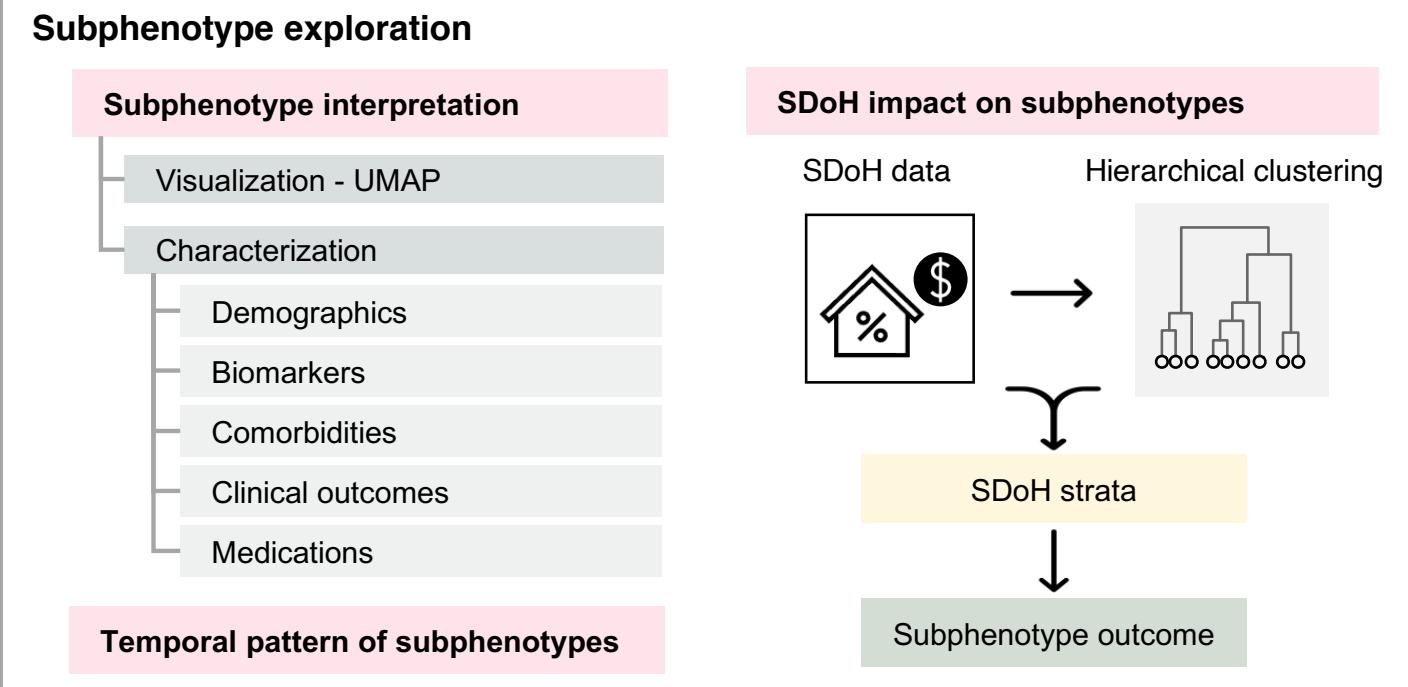
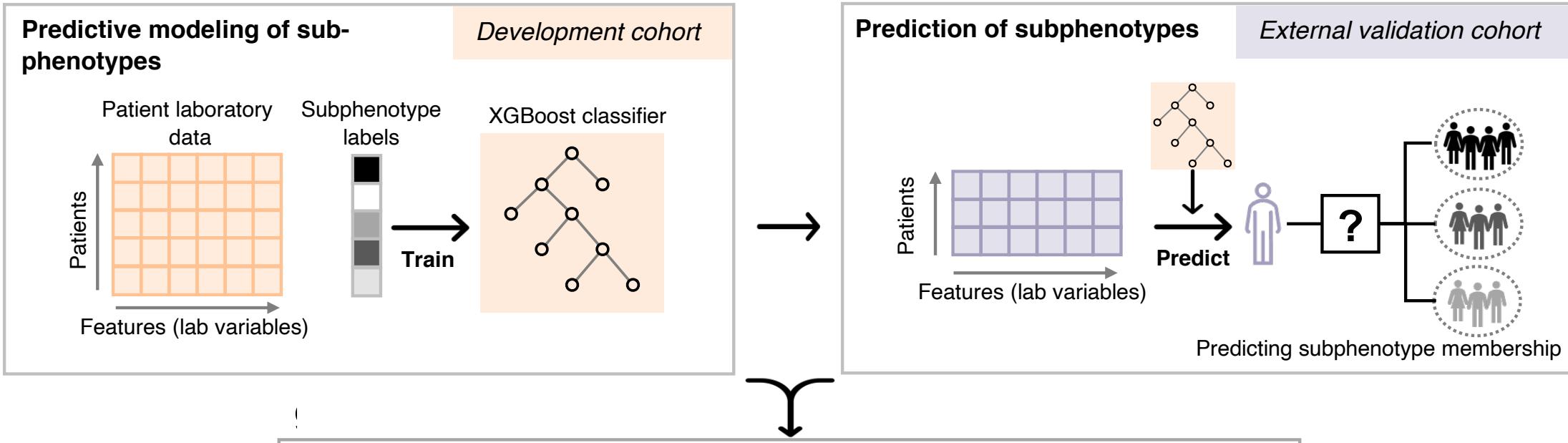
2. Sensitivity to clustering methods

Re-deriving subphenotypes using another clustering method - Gaussian mixture model.

Re-derivation

Internal validation cohort

Re-deriving subphenotypes in internal validation cohort using agglomerative hierarchical clustering.

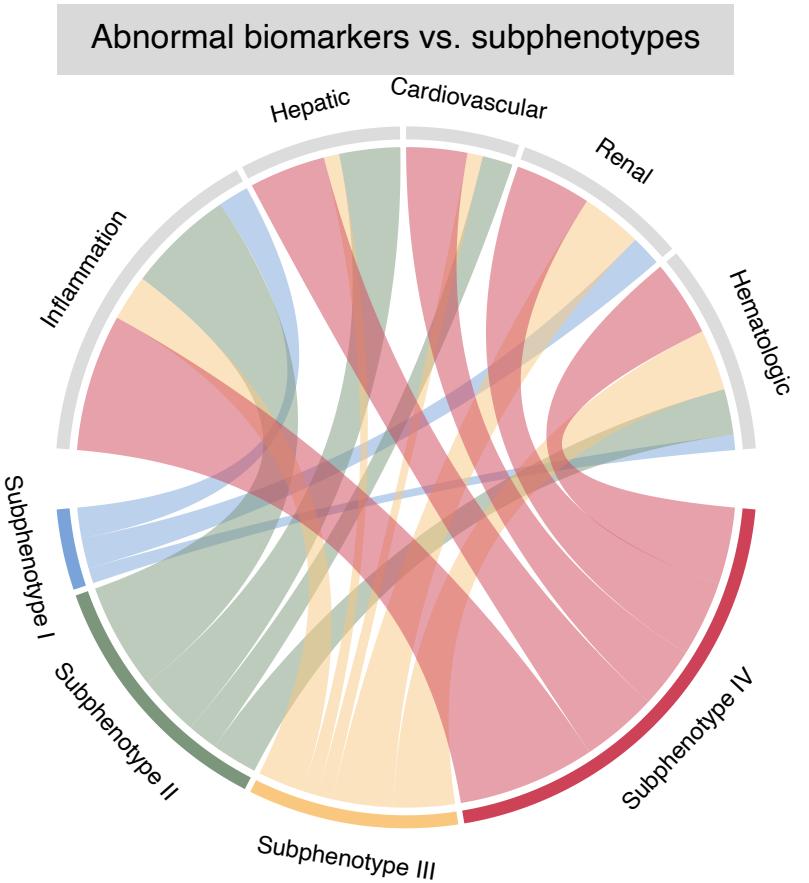


Cohort Characteristics

Characteristics	Cohort		
	Development cohort	Internal validation cohort	External validation cohort
No. of patients	8,199	3,519	2,700
Construction method	70% patients (randomly selected) from 4 sites of INSIGHT network: NYU-LMC, NYP-WCMC, MSHS, and MMC	Remaining 30% patients from 4 sites of INSIGHT network: NYU Langone Medical Center, NYP-WCMC, Mount Sinai Health System, and Montefiore Medical Center	NYP-CUMC
Age, y, Median (IQR)	63.53 [50.57 - 75.15]	63.51 [50.95 - 75.17]	65.58 (51.08 - 77.39)
Sex female, N (%)	3,787 (46.2)	1,585 (45.0)	1,305 (48.3)
Race, N (%)			
White	2,036 (24.8)	838 (23.8)	675 (25.0)
Black	2,155 (26.3)	915 (26.0)	545 (20.2)
Asian	409 (5.0)	193 (5.5)	28 (1.0)
Multiple race	39 (0.5)	13 (0.4)	912 (33.8)
Other/unknown	3560 (43.4)	1560 (44.3)	540 (20.0)
Outcomes (60 days), N (%)			
Mortality	1529 (18.65)	696 (19.78)	556 (20.59)
Mechanical ventilation (intubation)	1154 (14.07)	497 (14.12)	248 (9.19)
ICU admission	1494 (18.22)	661 (18.78)	-

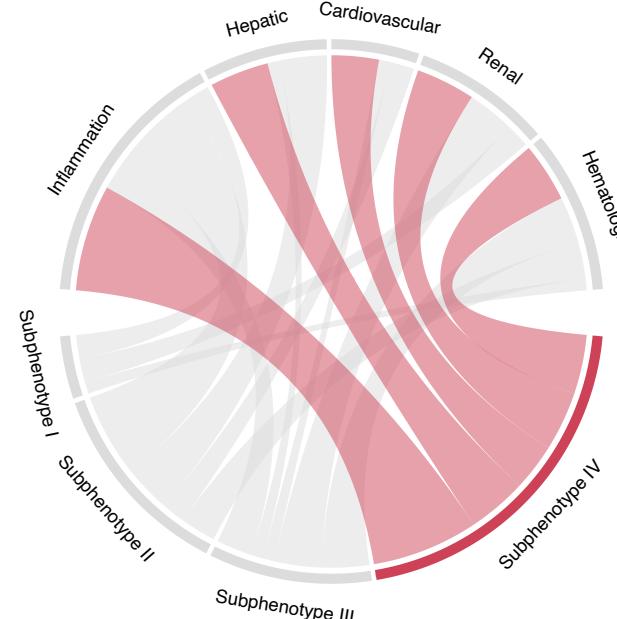
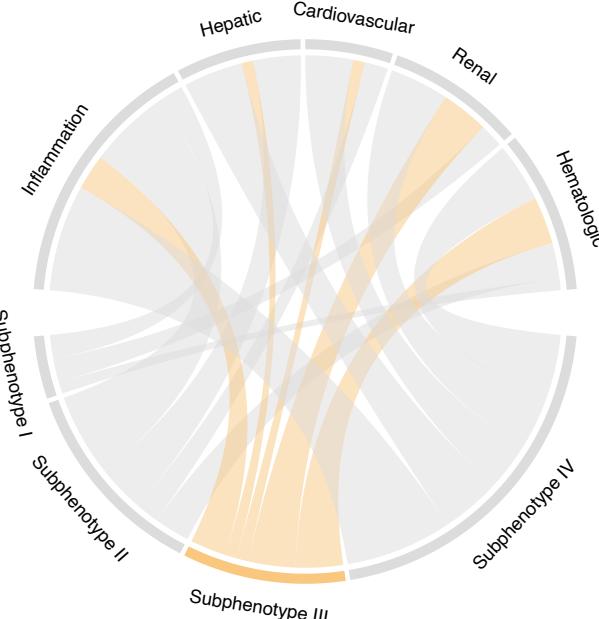
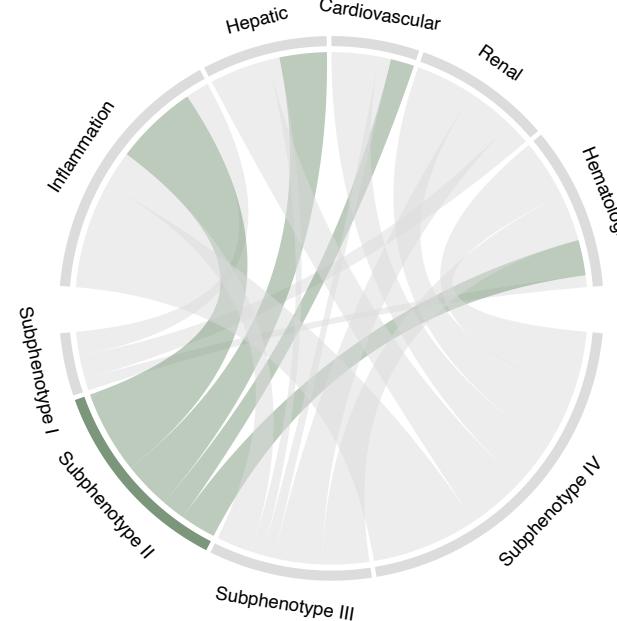
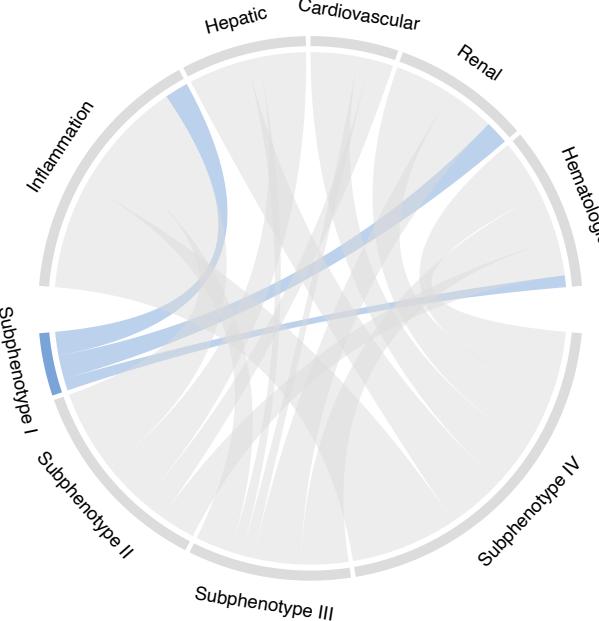
Abnormal biomarkers vs. Subphenotype I

Abnormal biomarkers vs. Subphenotype II

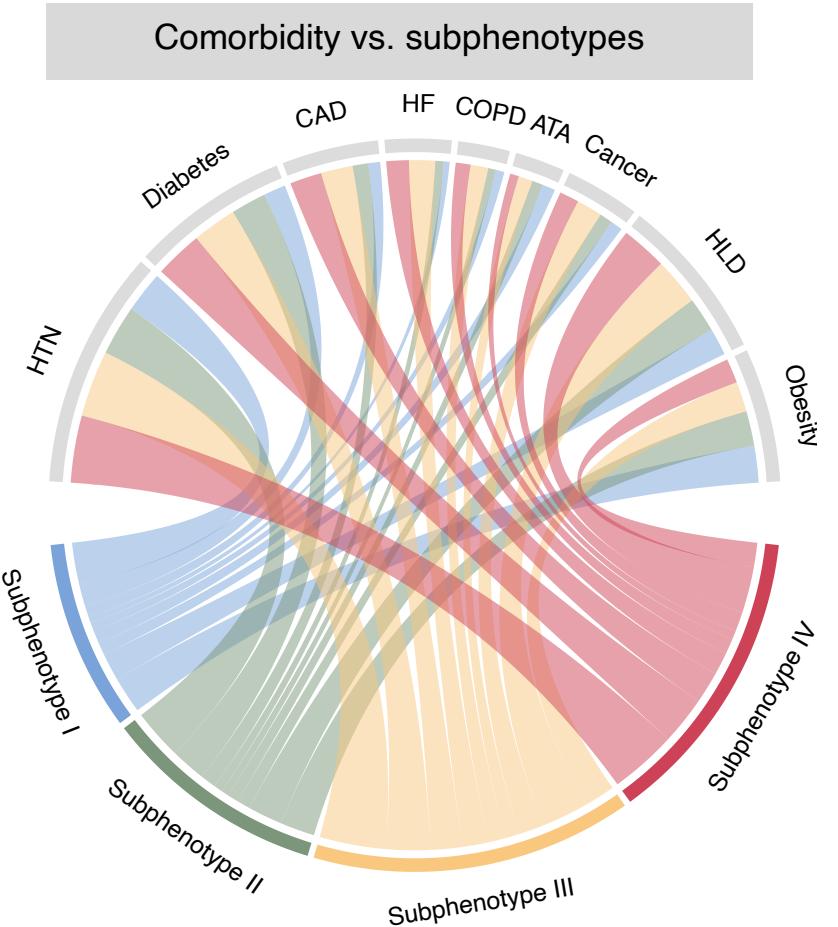


Abnormal biomarkers vs. Subphenotype III

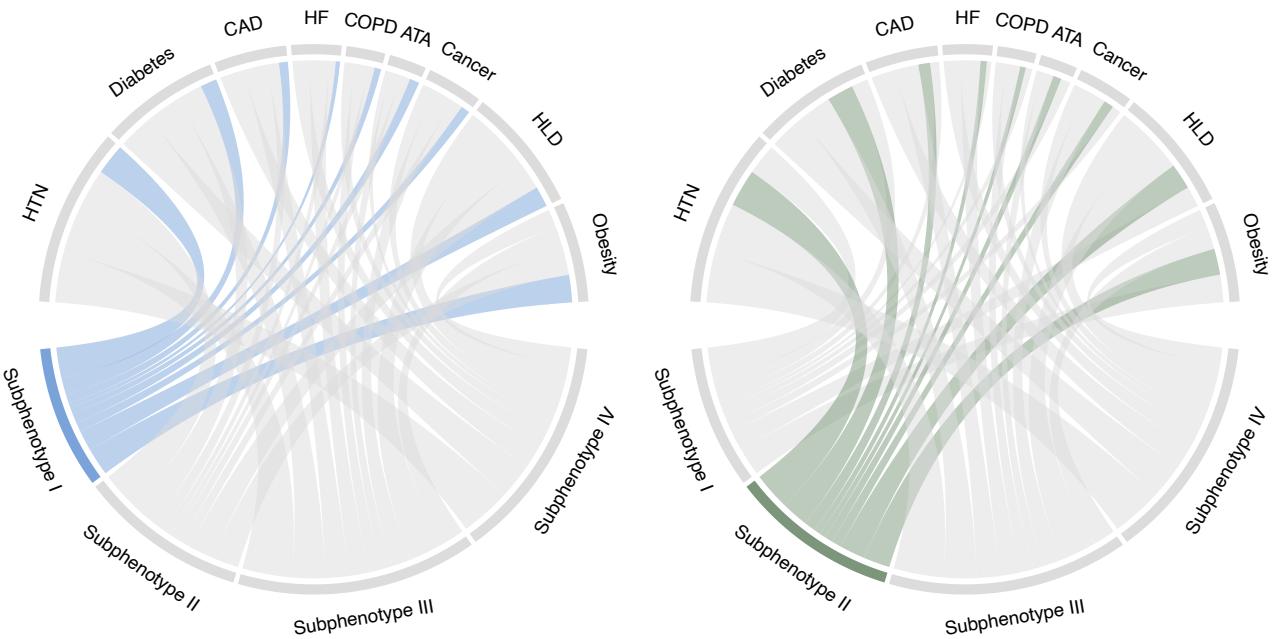
Abnormal biomarkers vs. Subphenotype IV



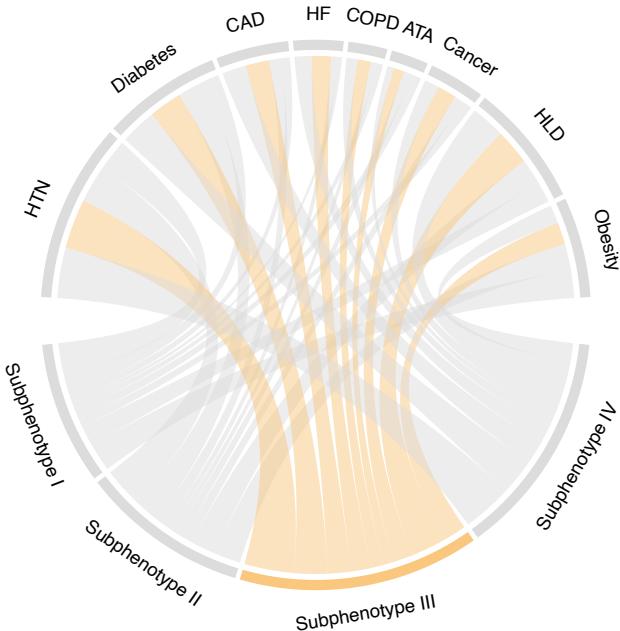
Comorbidity vs. Subphenotype I



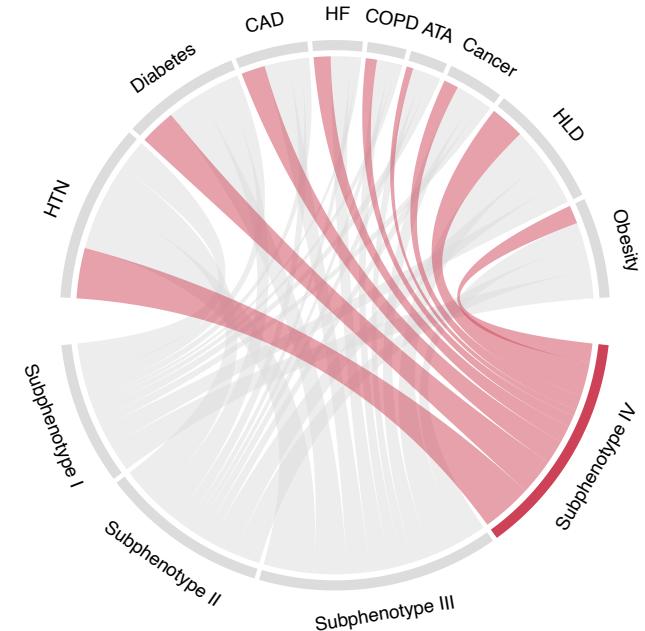
Comorbidity vs. Subphenotype II

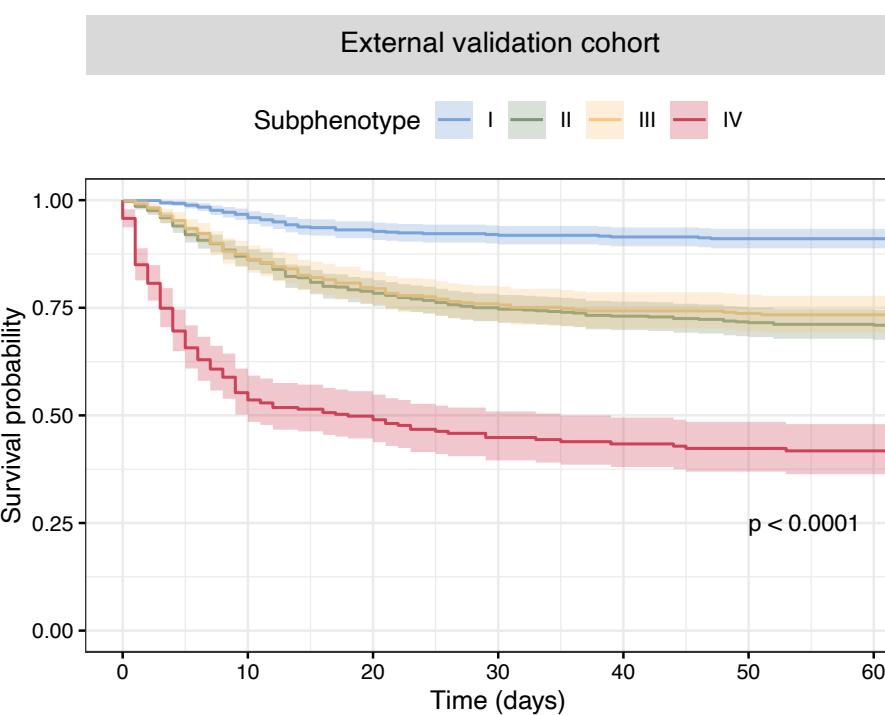
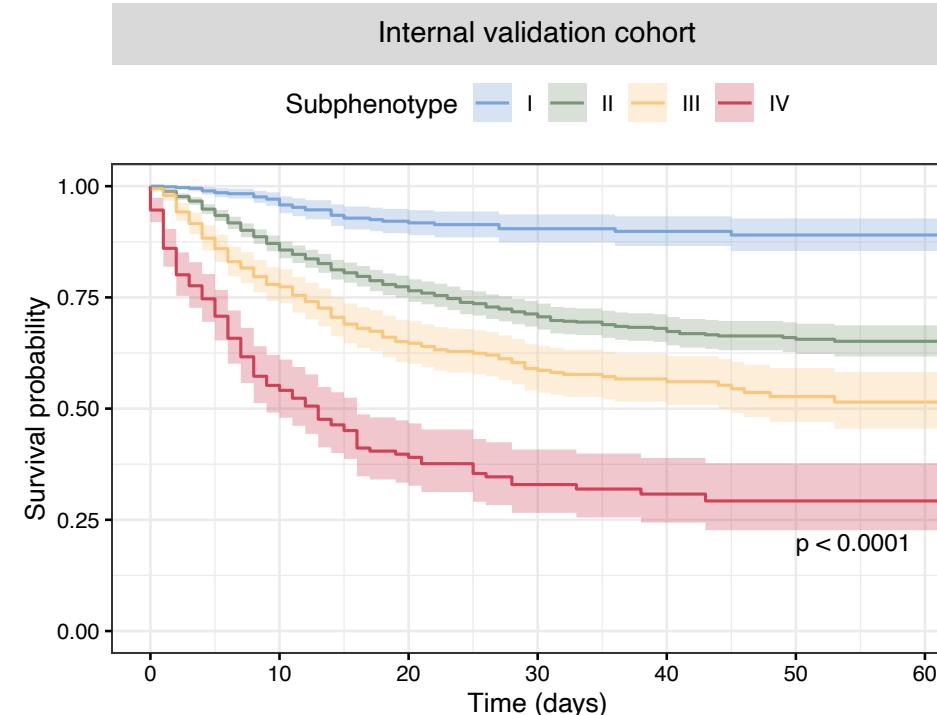
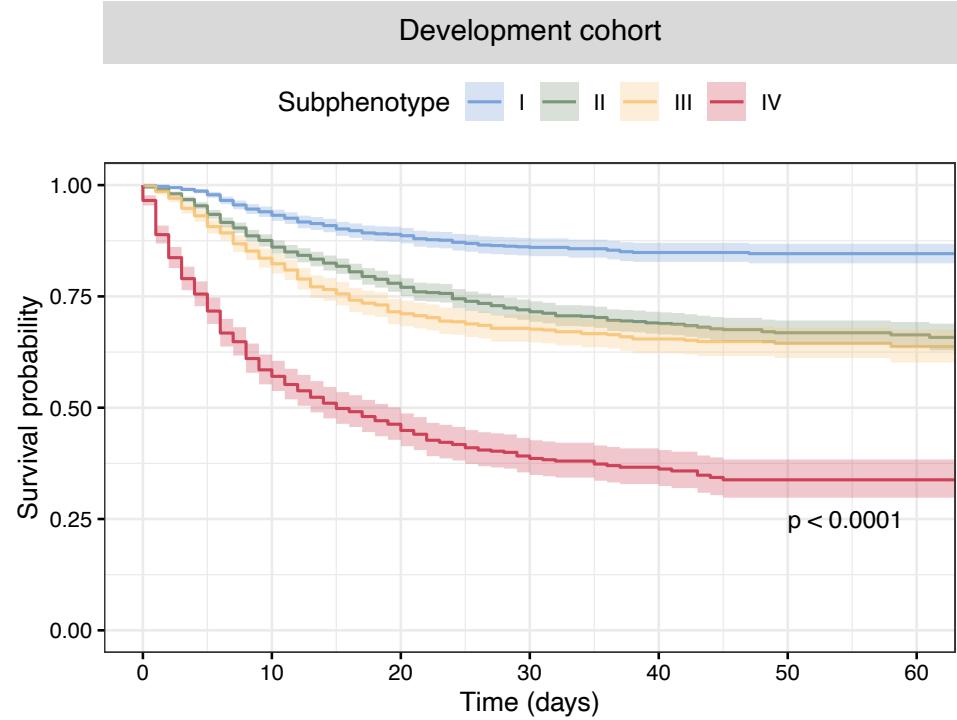


Comorbidity vs. Subphenotype III



Comorbidity vs. Subphenotype IV



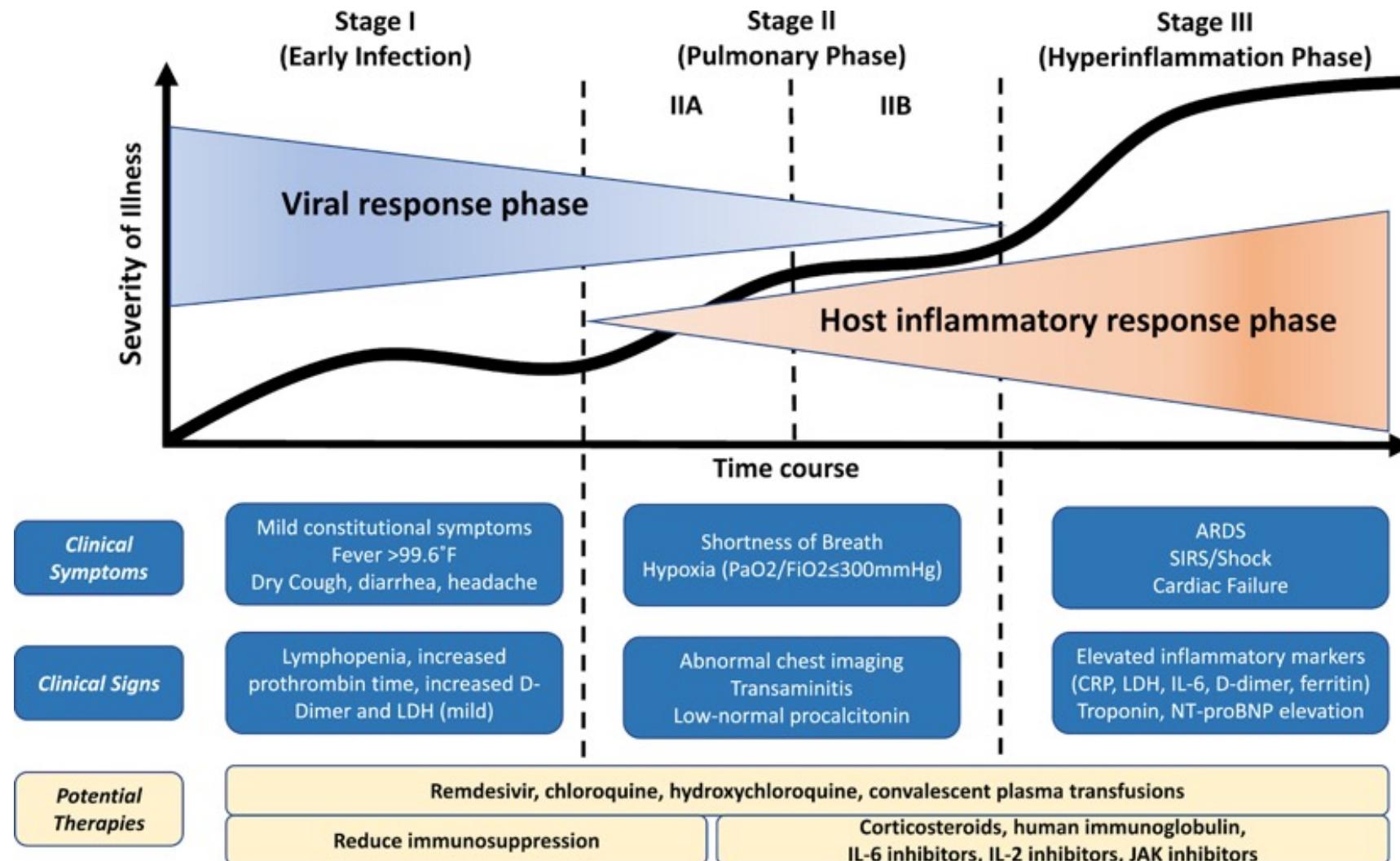


Outline

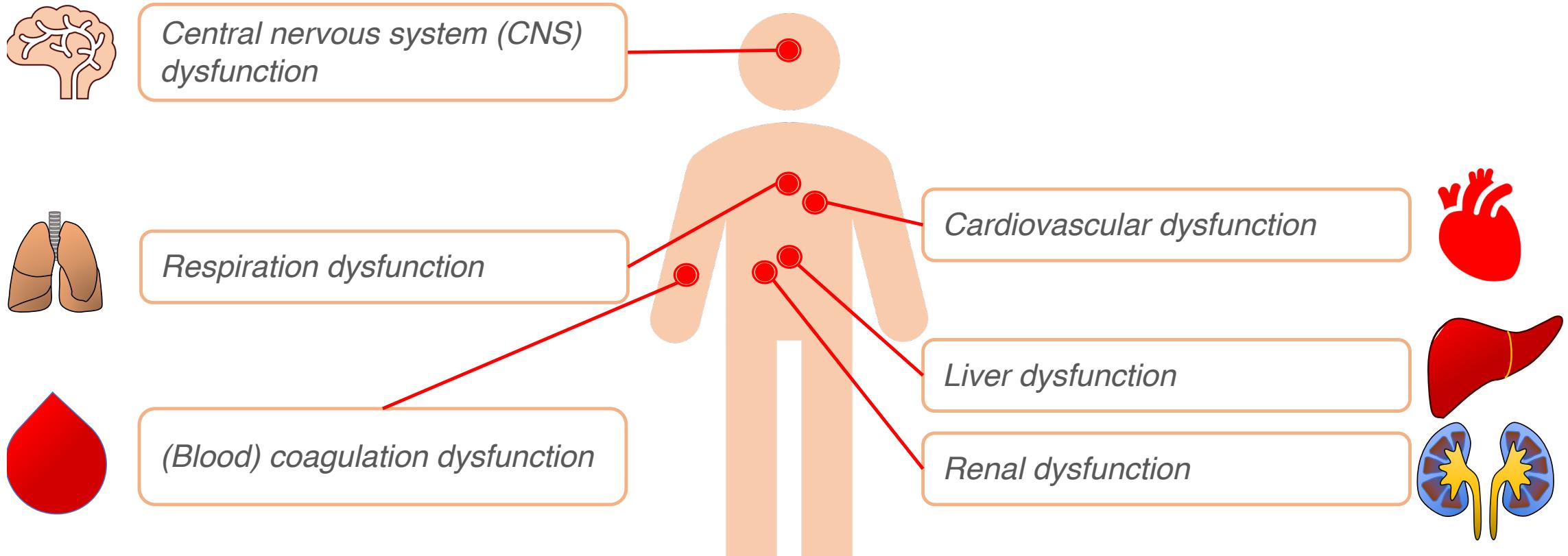
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- Subphenotyping of Long COVID
- Subphenotyping of PD
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Su, Chang, Zhenxing Xu, Katherine Hoffman, Parag Goyal, Monika M. Safford, Jerry Lee, Sergio Alvarez-Mulett et al. "Identifying organ dysfunction trajectory-based subphenotypes in critically ill patients with COVID-19." *Scientific Reports* 11, no. 1 (2021): 15872.

An Early Conceptual Model for the Progression of COVID-19 in Acute Phase



Sequential Organ Failure Assessment



Cohort Setup

Mar 1st to May 12th

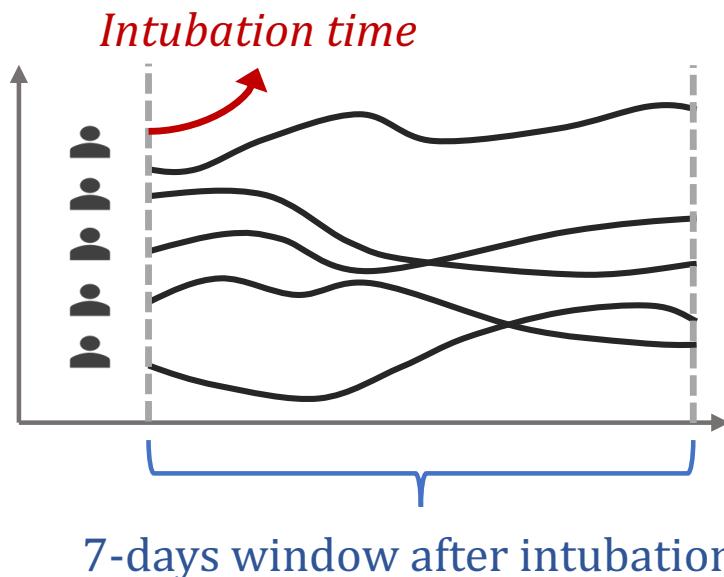
New York Presbyterian
Weill Cornell Medical Center
(NYP-WCMC) – **348 patients**

Development

New York Presbyterian
Lower Manhattan Hospital
(NYP-LMH) – **100 patients**

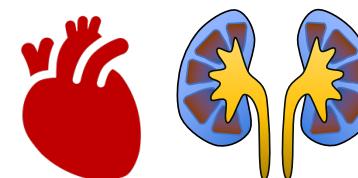
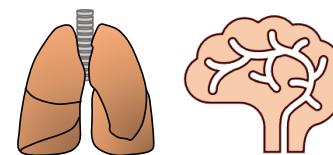
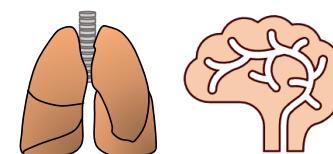
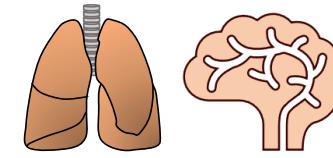
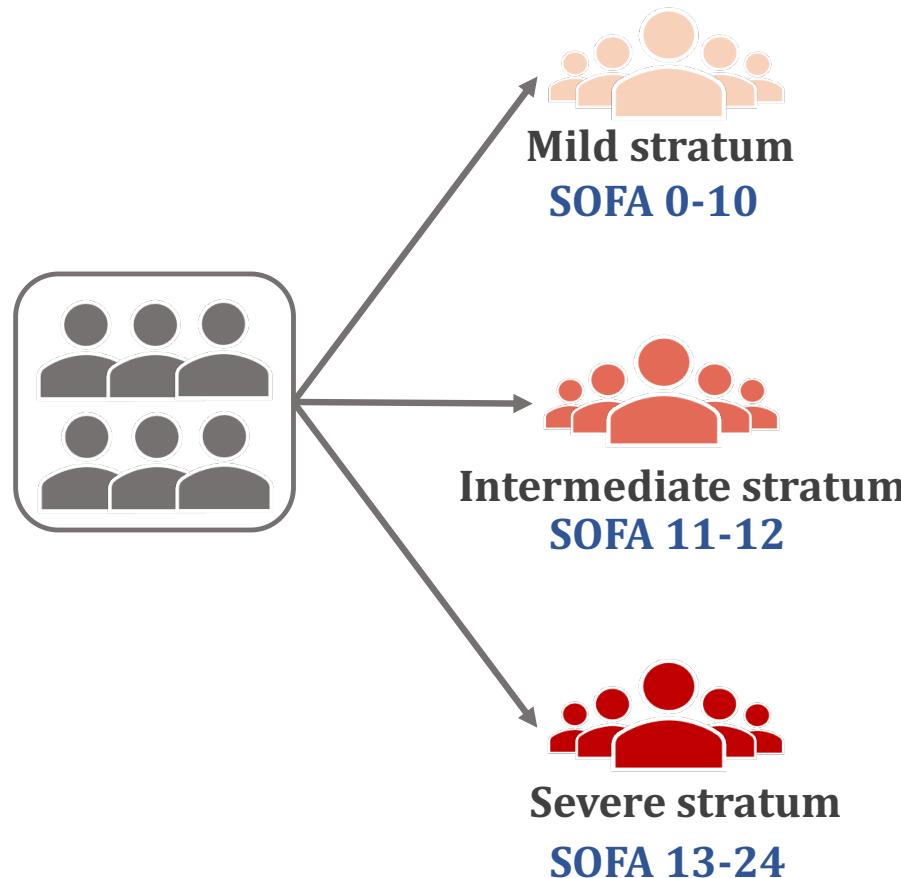
Validation

Post-intubation SOFA trajectory



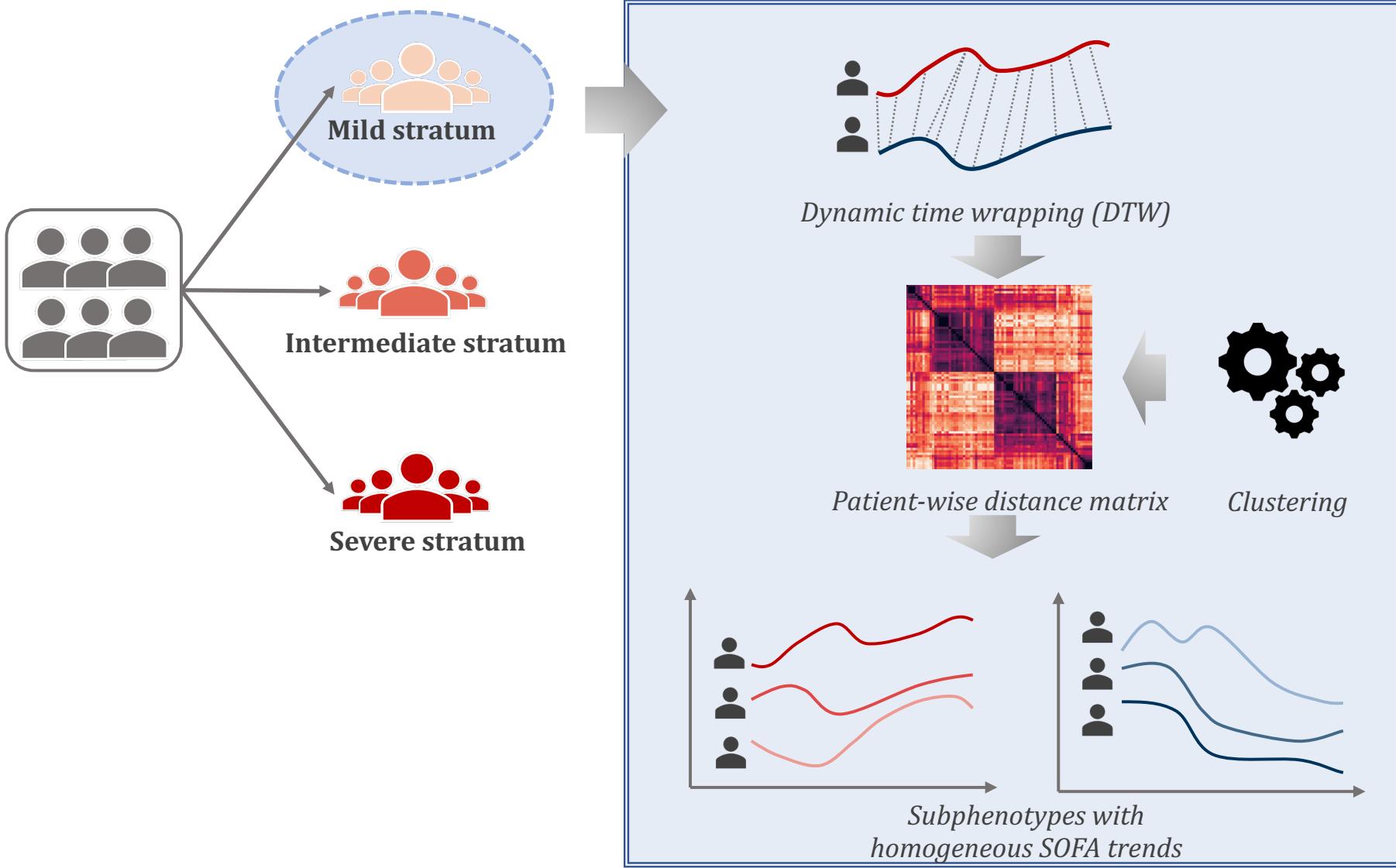
- SOFA scores were calculated every 24 hours
- Patients missing more than 3-days SOFA data were excluded

Baseline Stratification

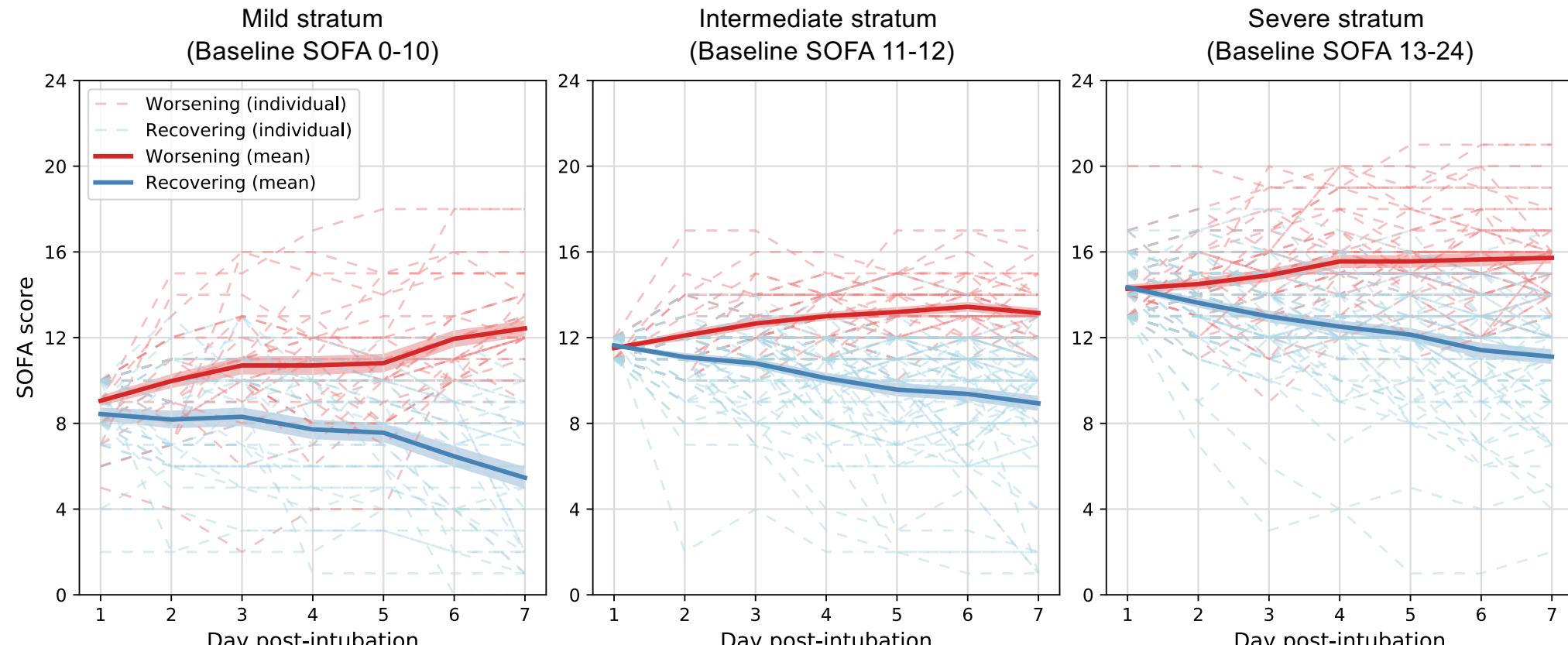


	Mild	Intermediate	Severe
Respiration SOFA	3.45 (0.89)	3.89 (0.45)	3.97 (0.25)
CNS SOFA	3.34 (1.13)	3.72 (0.47)	3.94 (0.24)
Cardiovascular SOFA	1.32 (1.34)	3.41 (0.88)	3.69 (0.70)
Renal SOFA	0.16 (0.54)	0.35 (0.67)	1.96 (1.44)
Liver SOFA	0.20 (0.46)	0.14 (0.43)	0.37 (0.67)
Coagulation SOFA	0.12 (0.40)	0.04 (0.20)	0.28 (0.64)

Trajectory Grouping



Identified Subphenotypes

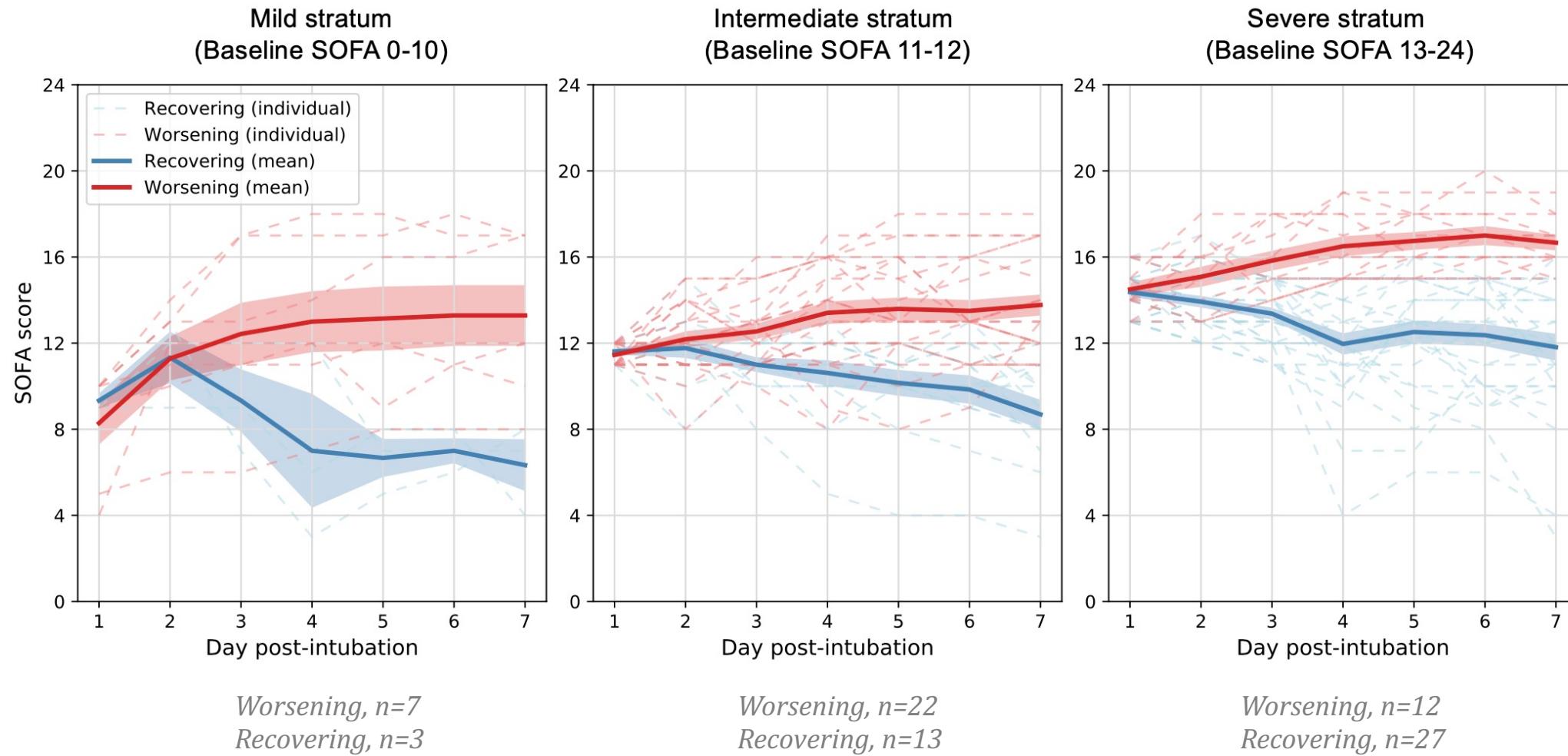


Worsening, n=37
Recovering, n=39

Worsening, n=41
Recovering, n=75

Worsening, n=54
Recovering, n=72

Identified Subphenotypes

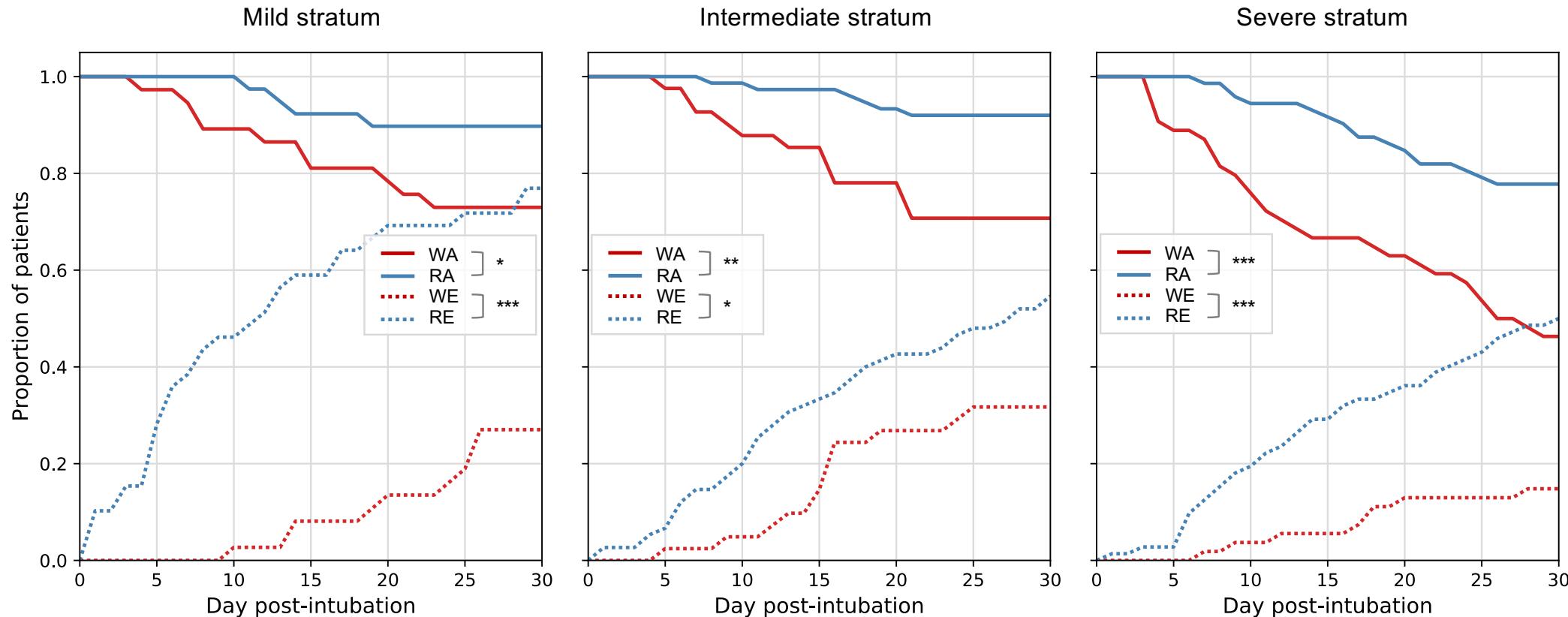


*Worsening, n=7
Recovering, n=3*

*Worsening, n=22
Recovering, n=13*

*Worsening, n=12
Recovering, n=27*

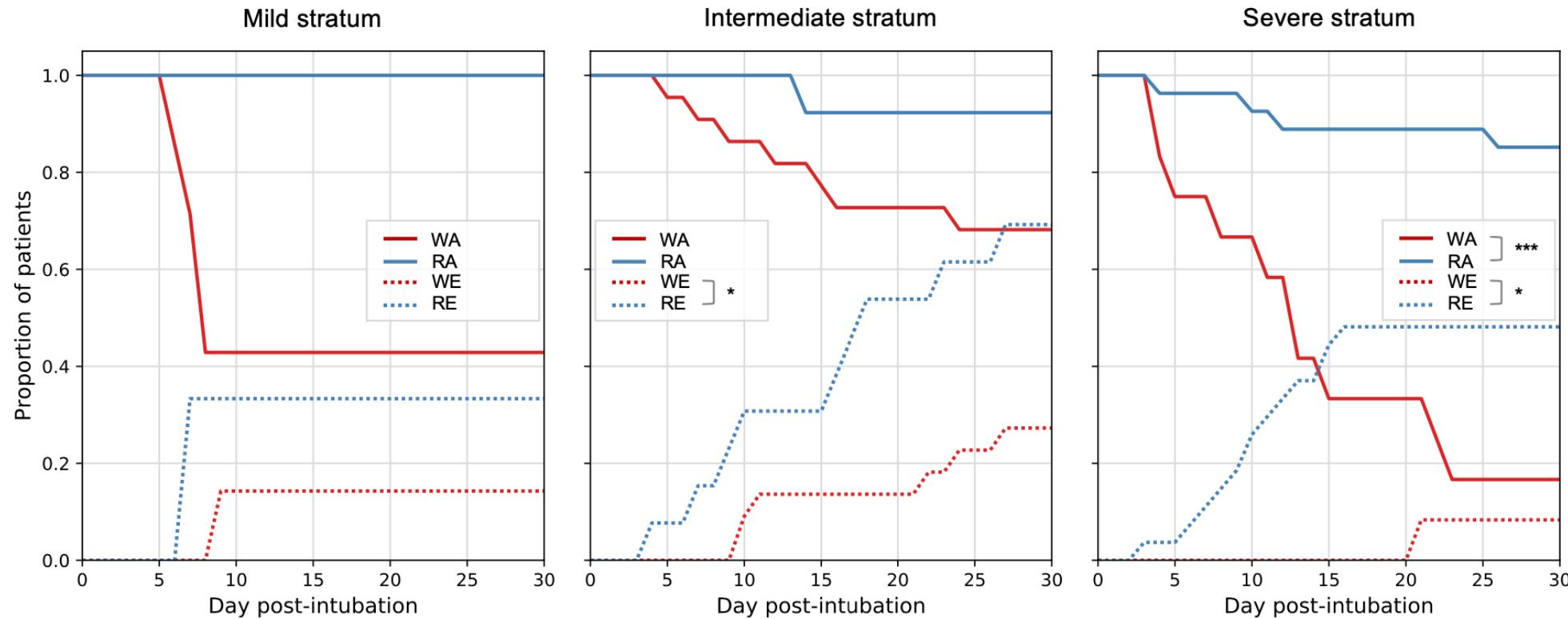
Association with Outcomes



* $P < 0.05$
** $p < 0.01$
*** $p < 0.001$

Abbreviations: WA=worsening subphenotype alive; RA=recovering subphenotype alive;
WE=worsening subphenotype extubated; RE=recovering subphenotype extubated.

Association with Outcomes



* $P < 0.05$

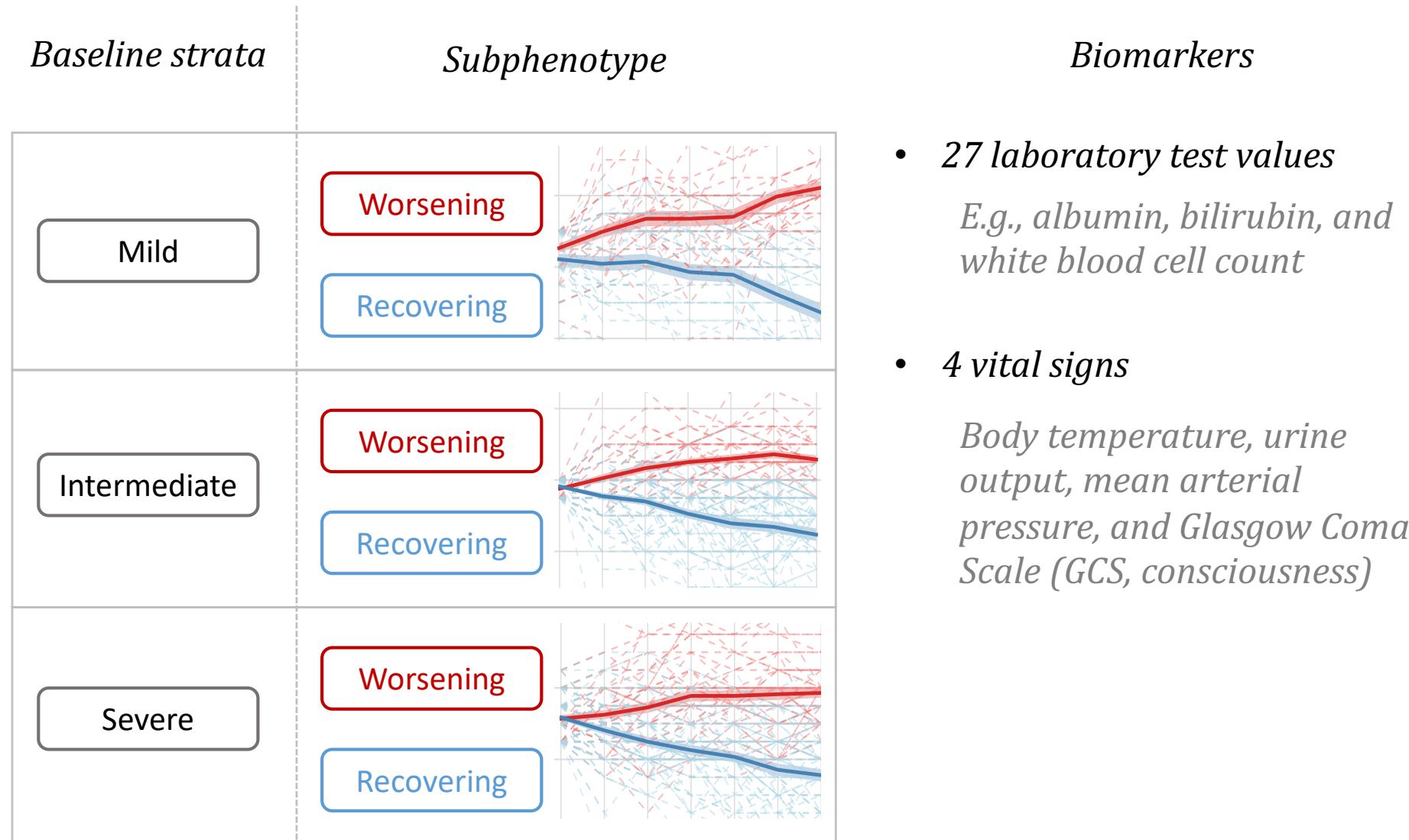
** $p < 0.01$

*** $p < 0.001$

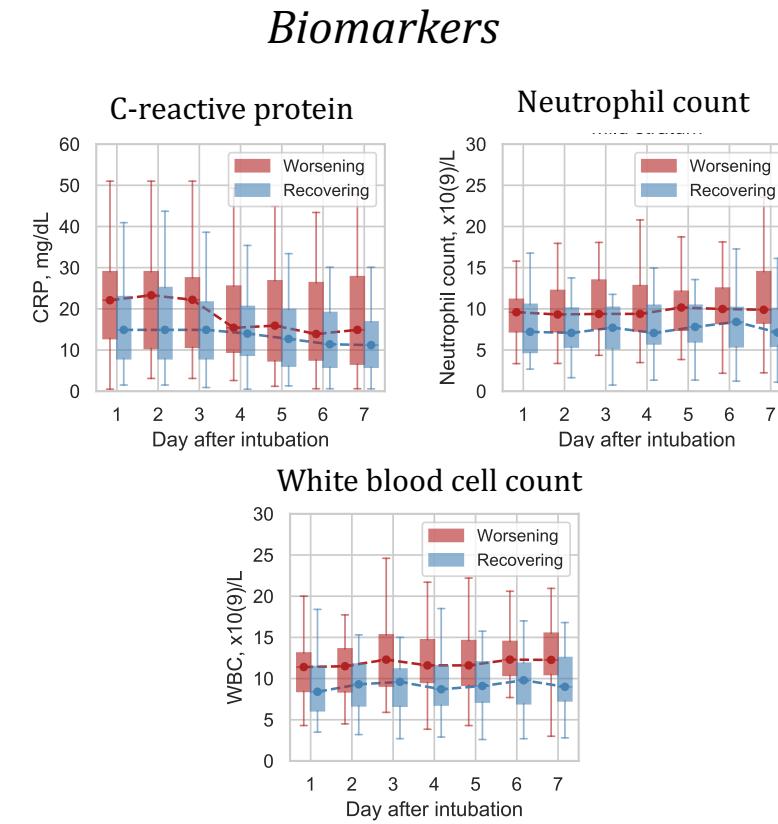
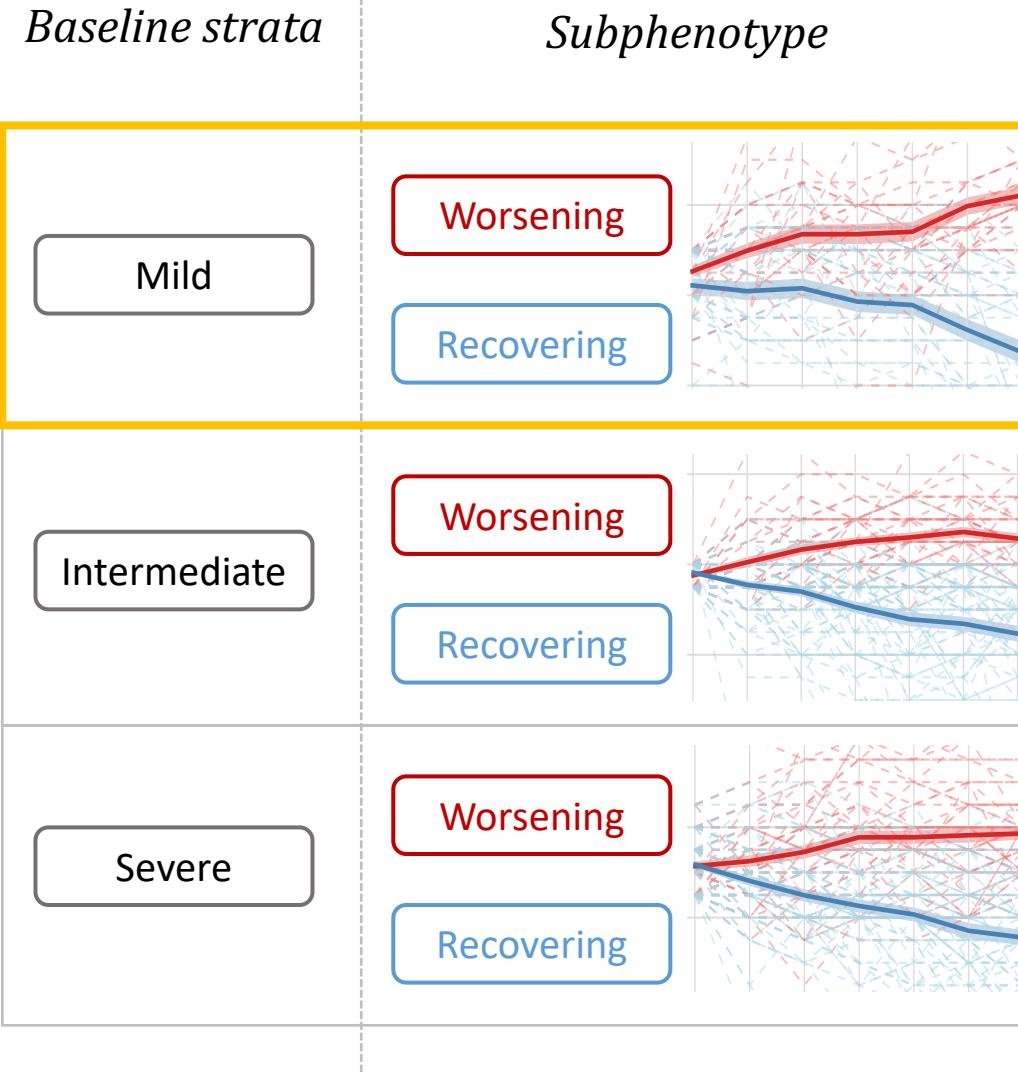
Abbreviations: WA=worsening subphenotype alive; RA=recovering subphenotype alive;

WE=worsening subphenotype extubated; RE=recovering subphenotype extubated.

Discriminative Biomarker Identification

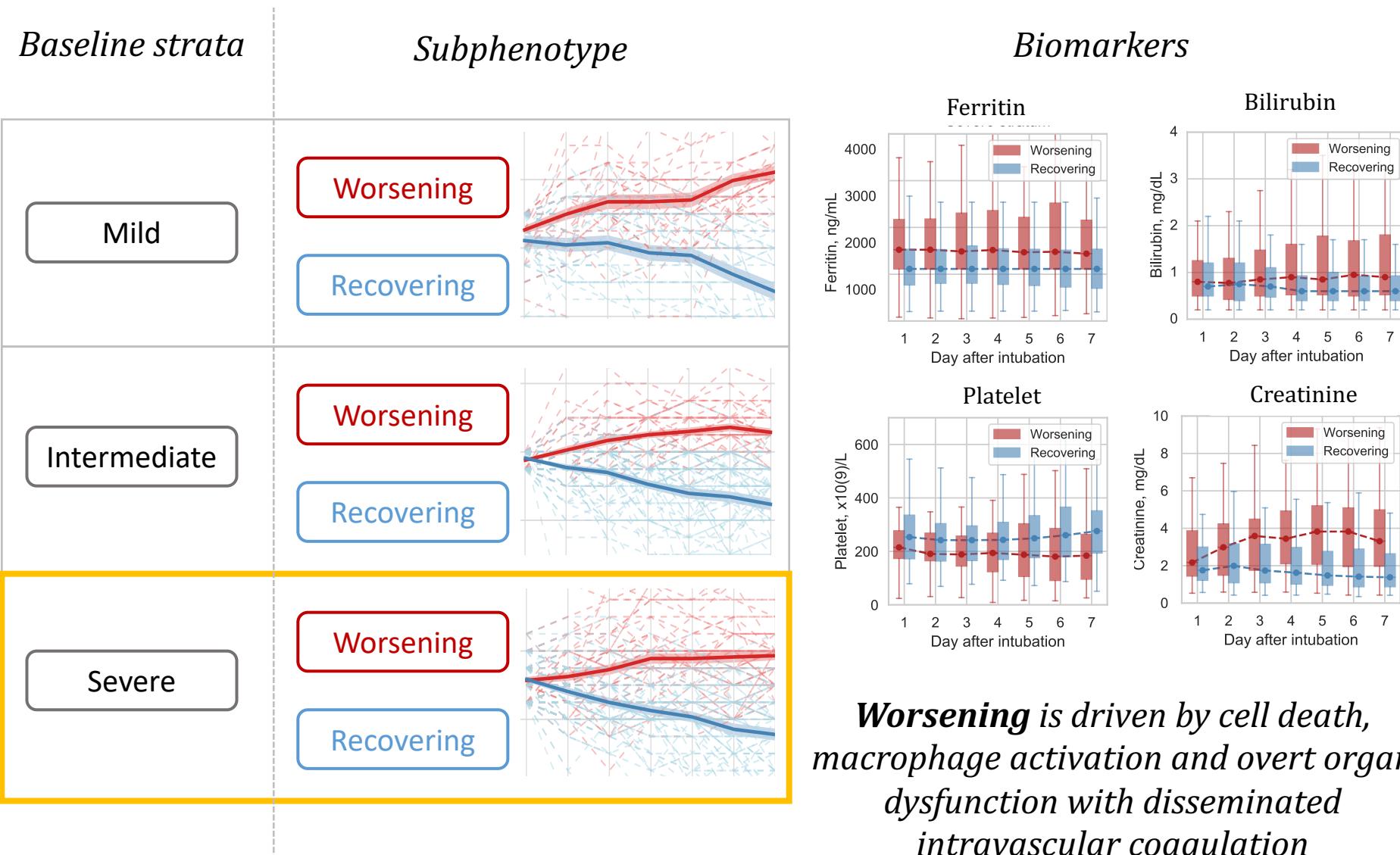


Discriminative Biomarker Identification



Inflammatory hinders the worsening subphenotype from recovery.

Discriminative Biomarker Identification



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Zhang, Hao, Chengxi Zang, Zhenxing Xu, Yongkang Zhang, Jie Xu, Jiang Bian, Dmitry Morozyuk et al. "Data-driven identification of post-acute SARS-CoV-2 infection subphenotypes." *Nature Medicine* 29, no. 1 (2023): 226-235.

Pipeline

DATABASE



Electronic Health Records (EHR) data for patients with lab-confirmed SARS-CoV-2 Infection from two clinical research networks (CRN)

- INSIGHT: New York City area
- OneFlorida+: Florida, Georgia and Alabama

METHOD

Cohort: SARS-CoV-2 infected patients with newly incident conditions within 30-180 days after infection

Variables: 137 investigative conditions

	1	0	0	0	0	0	0
Anemia	1	0	0	0	0	0	0
Circulatory problem	1	0	0	0	0	0	0
Disorders of stomach	0	1	0	0	0	0	0
Malaise and fatigue	0	1	1	0	0	1	0
Nausea and Vomiting	1	1	0	0	0	0	0
Headache	0	0	1	0	0	0	0
Respirator problem	0	0	0	1	0	0	0
⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
Musculoskeletal pain	0	0	0	0	0	0	1
Osteoarthritis	0	0	0	0	0	0	1

Step 1. Binary vector representations of patients with incident PASC diagnosis

Topic 1	PASC	Weight
	Disorders of stomach	0.32
	Nausea and Vomiting	0.23
	Esophageal disorders	0.20
⋮	⋮	⋮
Topic 2	PASC	Weight
	Anemia	0.36
	Heart failure	0.25
	Cardiac dysrhythmias	0.19
⋮	⋮	⋮
Topic K	PASC	Weight
	Musculoskeletal pain	0.34
	Osteoarthritis	0.28
	Spondylopathies	0.14
⋮	⋮	⋮

Step 2. Inference of PASC topics. Each PASC topic encodes a particular set of frequently co-occurred incident PASC diagnosis

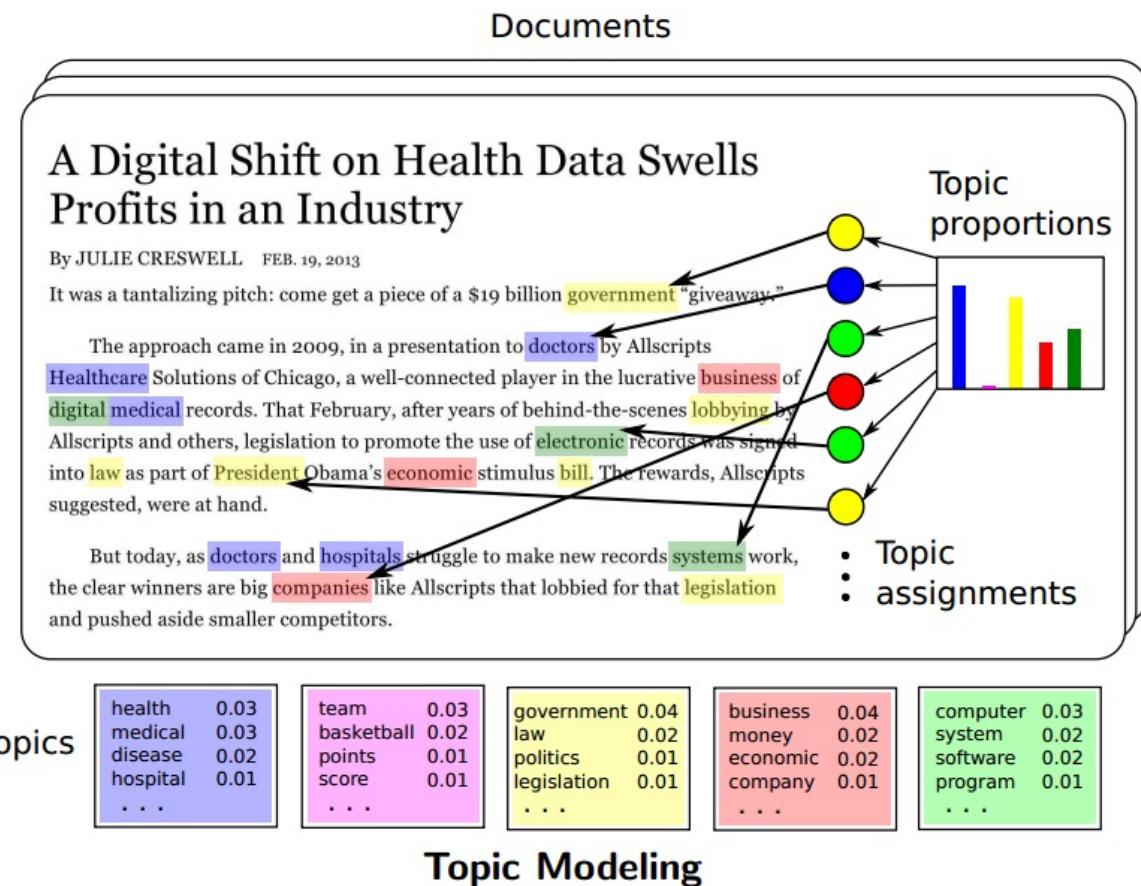
Topic 1	0.05	0.74	0.08	0.02
Topic 2	0.65	0.01	0.13	0.06
⋮	⋮	⋮	⋮	⋮
Topic K-1	0.12	0.03	0.53	0.03
Topic K	0.07	0.10	0.02	0.69

Step 3. Derivation of the patient representation in the PASC topic space



Step 4. Derivation of the PASC subphenotypes as patient groups with the PASC topic-based representation through cluster analysis.

Background – probabilistic topic modeling



➤ **Topics:** a distribution over all words. Global parameters shared by all documents.

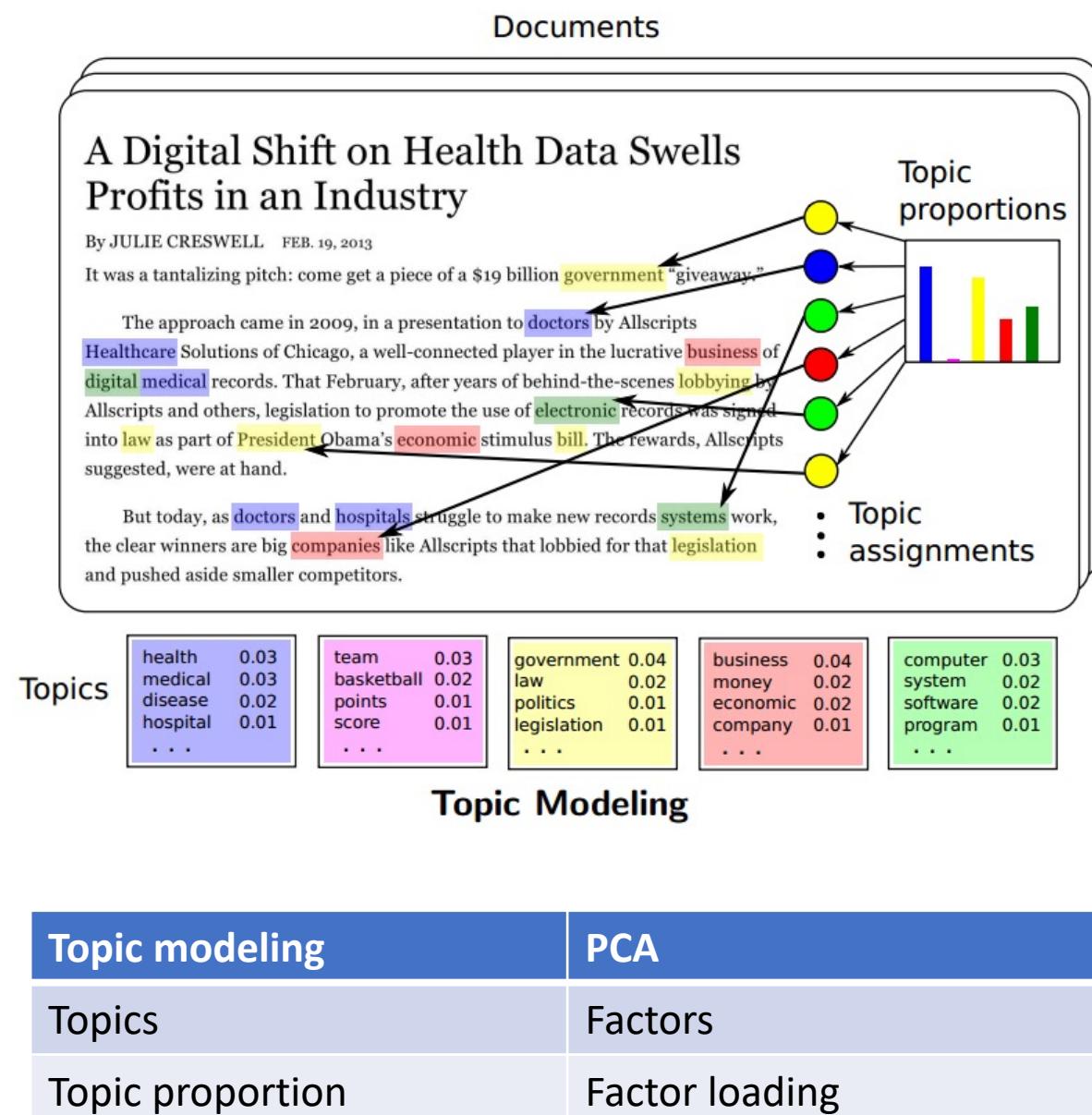
➤ **Topic proportion:** represent the importance of each topic in representing this document. Local parameters denotes the new feature of each document in topic space.

Transform the document represented by words to a new feature represented by topics.

The basic idea of topic modeling: exploring different topics (group of some “similar” words) for documents

Similar (word cooccurrence): some words should often appear simultaneously in one document

Background – probabilistic topic modeling



Transform the document represented by words to a new feature represented by topics.

Vocabulary	1)	2)
industry	3	0
NBA	0	6
economy	2	1
economic	3	2
game	0	5
medical	2	0
business	3	4

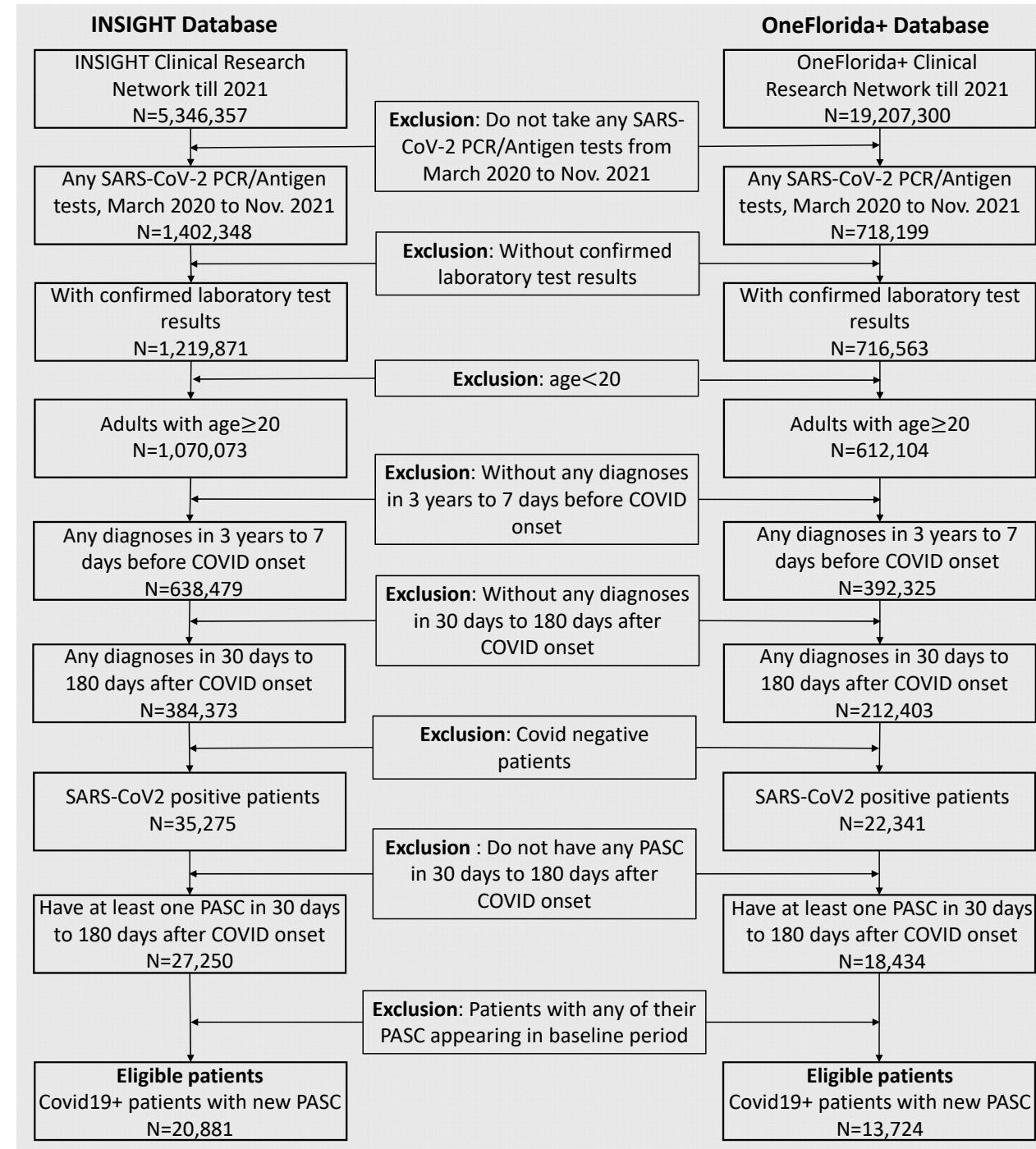
VS

Vocabulary	1)	2)
Topic1	0.4	0.05
Topic2	0.06	0.3
Topic3	0.3	0.04
Topic4	0.05	0.3
Topic5	0.19	0.31

This vector should be high-dimensional, sparse, and discrete.

This vector should be low-dimensional, dense, and continuous

Inclusion-Exclusion cascade

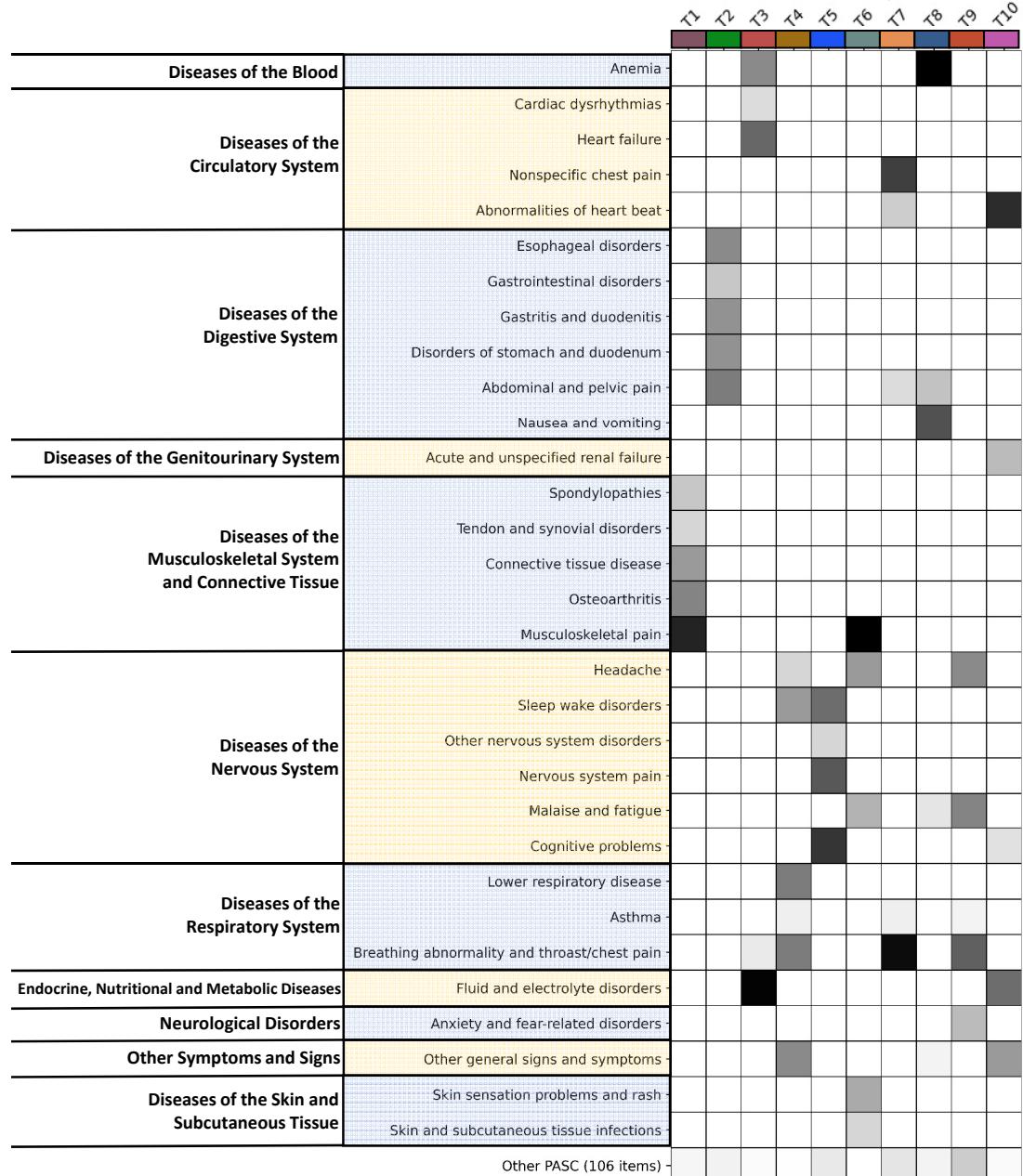


INSIGHT

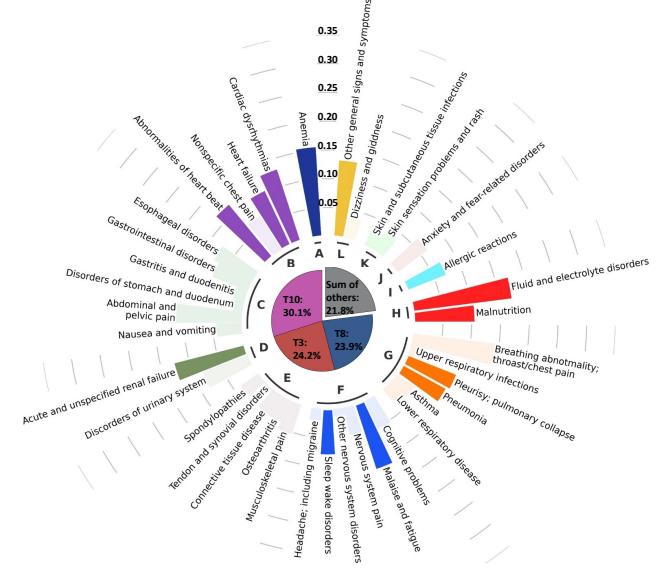
CCSR domain

PASC

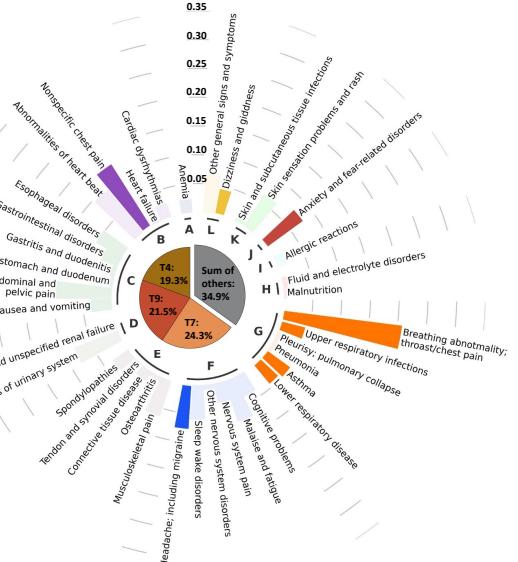
PASC Topic



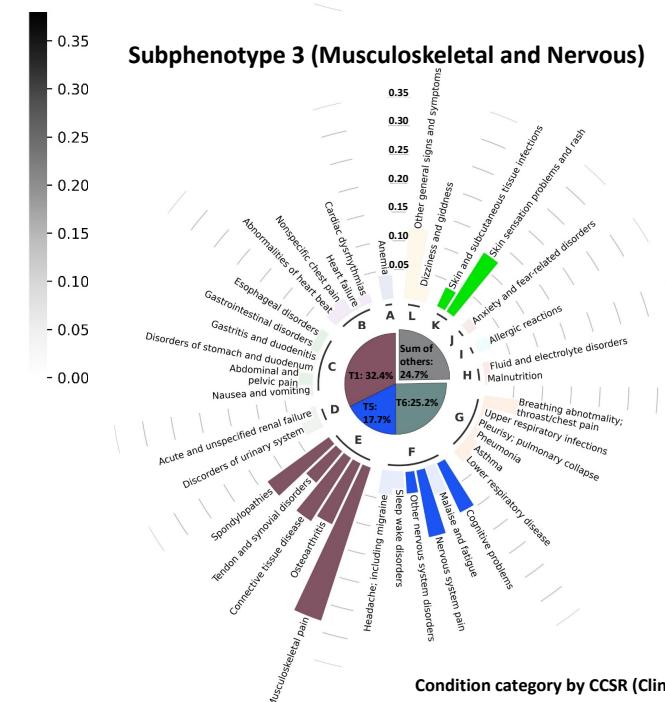
Subphenotype 1 (Cardiac and Renal)



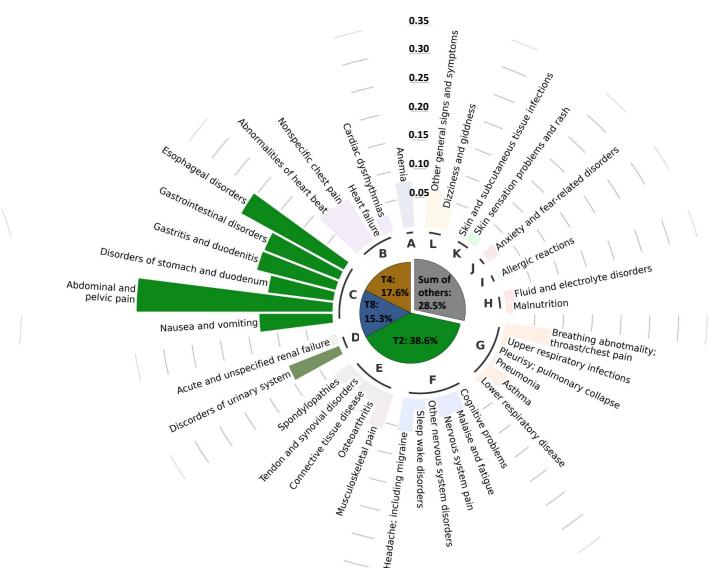
Subphenotype 2 (Respiratory, Sleep and Anxiety)



Subphenotype 3 (Musculoskeletal and Nervous)



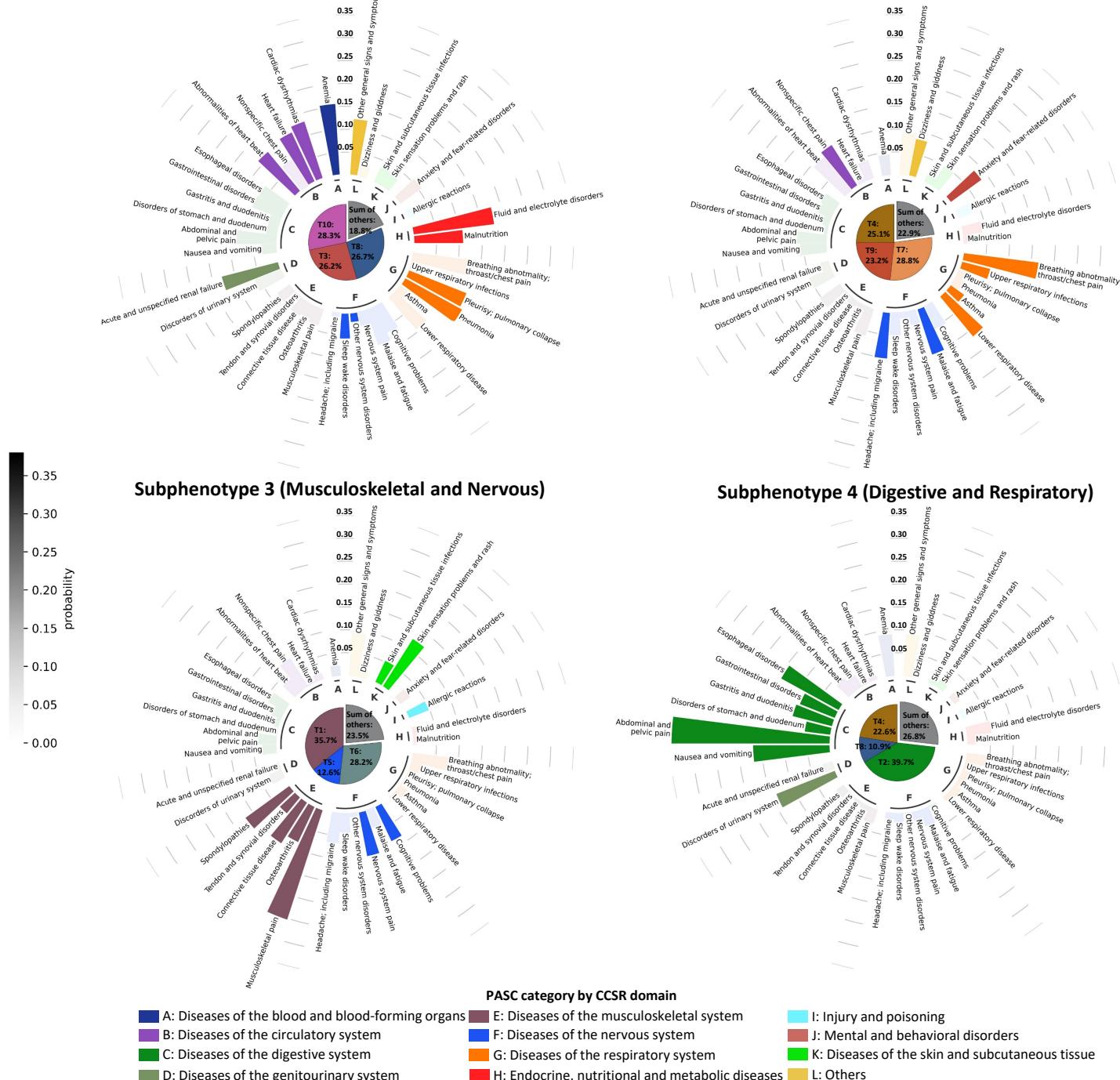
Subphenotype 4 (Digestive and Respiratory)



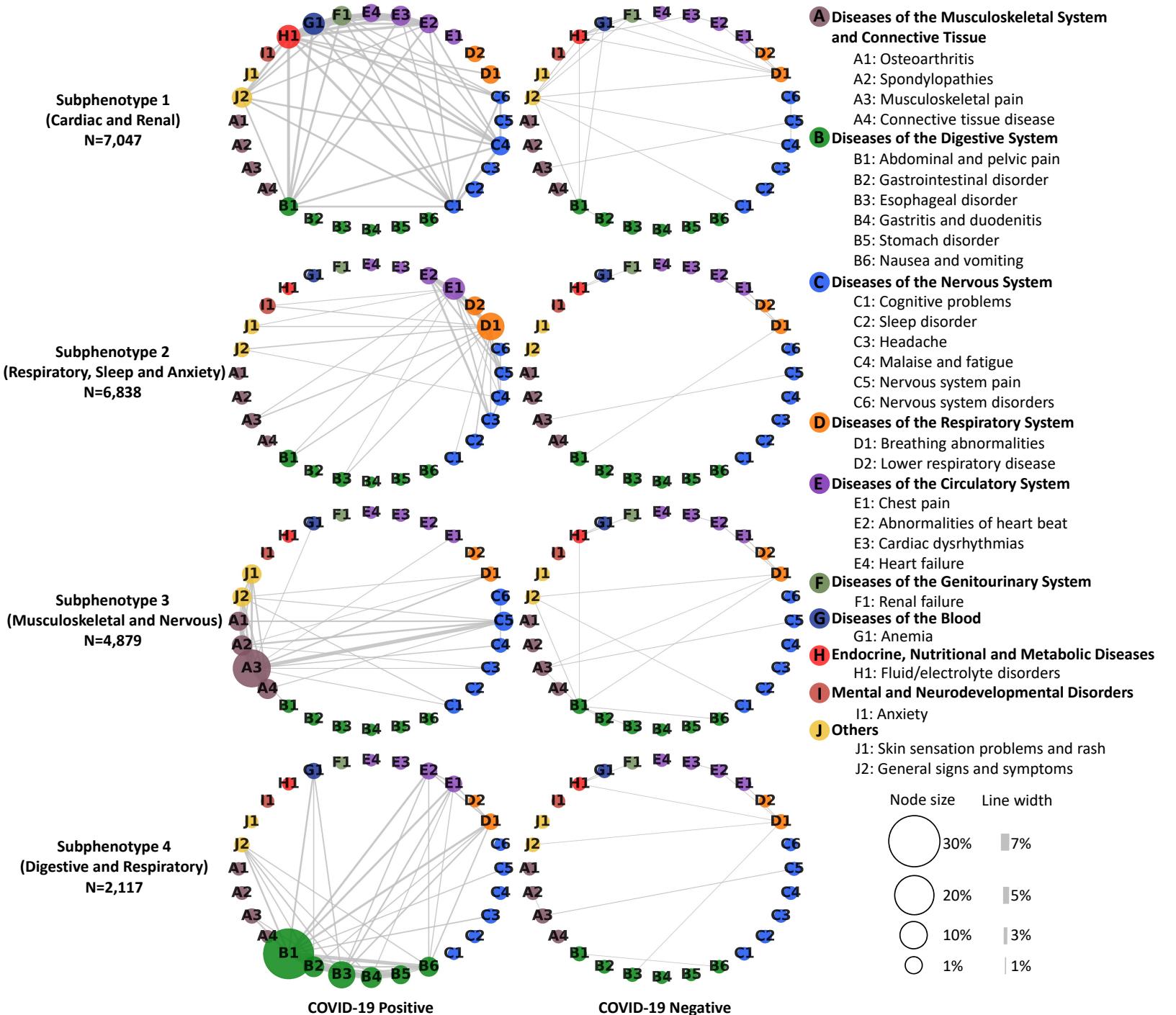
Condition category by CCSR (Clinical Classifications Software Refined) domain

- A: Diseases of the blood and blood-forming organs
- B: Diseases of the circulatory system
- C: Diseases of the digestive system
- D: Diseases of the genitourinary system
- E: Diseases of the musculoskeletal system
- F: Diseases of the nervous system
- G: Diseases of the respiratory system
- H: Endocrine, nutritional and metabolic diseases
- I: Injury and poisoning
- J: Mental and behavioral disorders
- K: Diseases of the skin and subcutaneous tissue
- L: Others

OneFlorida+



INSIGHT



OneFlorida+

Subphenotype 1
(Cardiac and Renal)
N=3,490

Subphenotype 2
(Respiratory, Sleep and Anxiety)
N=5,281

Subphenotype 3
(Musculoskeletal and Nervous)
N=3,205

Subphenotype 4
(Digestive and Respiratory)
N=1,748

COVID-19 Positive

COVID-19 Negative

A Diseases of the Musculoskeletal System and Connective Tissue

- A1: Osteoarthritis
- A2: Spondylopathies
- A3: Musculoskeletal pain
- A4: Connective tissue disease

B Diseases of the Digestive System

- B1: Abdominal and pelvic pain
- B2: Gastrointestinal disorder
- B3: Esophageal disorder
- B4: Gastritis and duodenitis
- B5: Stomach disorder
- B6: Nausea and vomiting

C Diseases of the Nervous System

- C1: Cognitive problems
- C2: Sleep disorder
- C3: Headache
- C4: Malaise and fatigue
- C5: Nervous system pain
- C6: Nervous system disorders

D Diseases of the Respiratory System

- D1: Breathing abnormalities
- D2: Lower respiratory disease

E Diseases of the Circulatory System

- E1: Chest pain
- E2: Abnormalities of heart beat
- E3: Cardiac dysrhythmias
- E4: Heart failure

F Diseases of the Genitourinary System

- F1: Renal failure

G Diseases of the Blood

- G1: Anemia

H Endocrine, Nutritional and Metabolic Diseases

- H1: Fluid/electrolyte disorders

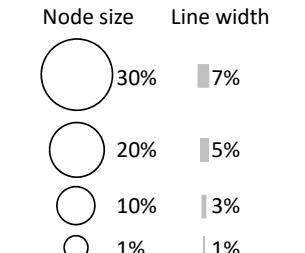
I Mental and Neurodevelopmental Disorders

- I1: Anxiety

J Others

- J1: Skin sensation problems and rash

- J2: General signs and symptoms



Outline

- Introduction
- Subphenotyping of COVID-19 at infection confirmation
- Subphenotyping of Severe COVID-19 after Mechanical Ventilation
- Subphenotyping of Long COVID
- **Discussions**

Discussions

- Complicated diseases are heterogeneous
 - Snapshot
 - Longitudinal
- Identification of disease subphenotypes from patients' clinical data can help us better understand the clinical heterogeneity and trigger stratified medicine
- The next step is to “validate” the subphenotypes
 - External validation on independent data
 - Mechanism investigation
 - Treatment response assessments

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<https://wcm-wanglab.github.io/index.html>

Thank You!!

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